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Remarks:

The complete document including Reference Tables and the Sequence Listing is available on CD-ROM from the European Patent Office, Vienne sub-office

(54) **Full-length cDNAs**

(57) Full-length cDNAs are provided.

1639 cDNA derived from human have been isolated. The full-length nucleotide sequences of the cDNA and amino acid sequences encoded by the nucleotide sequences have been determined. Because the cDNA

of the present invention are full-length and contain the translation start site, they provide information useful for analyzing the functions of the polypeptide.

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FIELD OF THE INVENTION

BACKGROUND OF THE INVENTION

20 [0003] However, determination of genomic sequences itself cannot identify the functions of all genes. For example, as for yeast, only the function of approximately half of the 6000 genes, which is predicted based on the genomic sequence, was able to be deduced. On the other hand, the human genome has been estimated to contain about 30,000-40,000 genes. Further, 100,000 or more types of mRNAs are said to exist when variants produced by alternative splicing are taken into consideration. Therefore, it is desirable to establish "a high throughput analysis system of the gene functions" which allows us to identify rapidly and efficiently the functions of vast amounts of the genes obtained by the genomic sequencing.

[0005] The information of ESTs is utilized for analyzing the structure of human genome, or for predicting the exons of genomic sequences or their expression profile. However, many human ESTs have been derived from proximal regions to the 3'-end of cDNA, and information around the 5'-end of mRNA is extremely little. Among human cDNAs, the number of the corresponding mRNAs whose encoding full-length protein sequences are deduced is approximately 13,000.

[0066] It is possible to identify the transcription start site of mRNA on the genomic sequence based on the 5'-end sequence of a full-length cDNA, and to analyze factors involved in the stability of mRNA that is contained in the cDNA, or in its regulation of expression at the translation stage. Also, since a full-length cDNA contains at least one start codon, the translation start site, in the 5'-region, it can be translated into a protein in a correct frame. Therefore, it is possible to produce a large amount of the protein encoded by the cDNA or to analyze biological activities of the expressed protein by utilizing an appropriate expression system. Thus, analysis of a full-length cDNA provides valuable information which complements the information from genome sequencing. Also, full-length cDNA clones that can be expressed are extremely valuable in empirical analysis of gene function and in industrial application.

45 [0007] Therefore, if a novel human full-length cDNA is isolated, it can be used for developing medicines for diseases in which the gene is involved. The protein encoded by the gene can be used as a drug by itself. Thus, it has great significance to obtain a full-length cDNA encoding a novel human protein.

[0008] In particular, human secretory proteins or membrane proteins would be useful by itself as a medicine like tissue plasminogen activator (TPA), or as a target of medicines like membrane receptors. In addition, genes for signal transduction-related proteins (protein kinases, etc.), glycoprotein-related proteins, transcription-related proteins, etc. are genes whose relationships to human diseases have been elucidated. Moreover, genes for disease-related proteins form a gene group rich in genes whose relationships to human diseases have been elucidated.

[0009] Therefore, it has great significance to isolate novel full-length cDNA clones of human, only few of which has been isolated. Especially, isolation of a novel cDNA clone encoding a secretory protein or membrane protein is desired since the protein itself would be useful as a medicine, and also the clones potentially include a gene involved in diseases. In addition, genes encoding proteins that are involved in signal transduction, glycoprotein, transcription, or diseases are expected to be useful as target molecules for therapy, or as medicines themselves. These genes form a gene group predicted to be strongly involved in diseases. Thus, identification of the full-length cDNA clones encoding those

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proteins has great significance.

SUMMARY OF THE INVENTION

[0010] An objective of the present invention is to provide polynucleotides encoding novel polypeptides, polypeptides encoded by the polynucleotides, and novel usages of these.

[0011] The inventors have developed a method for efficiently cloning, from a cDNA library having very high fullness-ratio, a human full-length cDNA that is predicted to be a full-length cDNA clone, where the cDNA library is synthesized by an improved method (WO 01/04286) of the oligo-capping method (K. Maruyama and S. Sugano, *Gene*, 138: 171-174 (1994); Y. Suzuki et al., *Gene*, 200: 149-156 (1997)). Then, the nucleotide sequences of cDNA clones whose fullness ratio is high, obtained by this method, were determined mainly from their 5'-ends, and, if required, from 3'-ends.

[0012] Further, representative clones, which were estimated to be novel and full-length, among the clones obtained, were analyzed for their full-length nucleotide sequences. The determined full-length nucleotide sequences were analyzed by BLAST homology search of the databases shown below. Because the homology search of the present invention is carried out based on the information of full-length cDNAs including the entire coding regions, homology to every part of a polypeptide can be analyzed. Thus, in the present invention, the reliability of homology search has been greatly improved.

[1] SwissProt

(http://www.ebi.ac.uk/ebi_docs/SwissProt_db/swishome.html),

[2] GenBank (<http://www.ncbi.nlm.nih.gov/web/GenBank>),

[3] UniGene (Human) (<http://www.ncbi.nlm.nih.gov/UniGene>), and

[4] nr (a protein database, which has been constructed by combining data of coding sequences (CDS) in nucleotide sequences deposited in GenBank, and data of SwissProt, PDB (<http://www.rcsb.org/pdb/index.html>), PIR (<http://pir.georgetown.edu/pirwww/pirhome.shtml>), and PRF (<http://www.prf.or.jp/en/>); overlapping sequences have been removed.)

[0013] Further, the gene expression profiles of cDNA clones whose full-length nucleotide sequence had been determined were studied by analyzing the large-scale cDNA database constructed based on the 5'-end nucleotide sequences of cDNAs obtained. In addition to the analysis for the expression profile by computer, the profiles of gene expression in living cells were also determined by PCR. The present inventors revealed the usefulness of the genes of the present invention based on these analysis results.

[0014] In the present invention, gene functions were revealed by the analysis of expression profiles *in silico* based on the information of full-length nucleotide sequences. The expression profiles used in the expression frequency analysis were studied based on the database containing sufficient amount of fragment sequence data. The expression frequency analysis was carried out by referring, for these expression profiles, to the full-length nucleotide sequences of many cDNA clones obtained in the present invention. Thus, a highly reliable analysis can be achieved by referring to the full-length nucleotide sequences of a wide variety of genes for the sufficiently large population for analysis (expression profiles). Namely, the results of expression frequency analysis using the full-length sequences of the present invention more precisely reflect the gene expression frequency in tissues and cells from which a certain cDNA library was derived. In other words, the information of full-length cDNA nucleotide sequence of the present invention made it possible to achieve the highly reliable expression frequency analysis.

[0015] The full-length cDNA clones of this invention were obtained by the method comprising the steps of [1] preparing libraries containing cDNAs with the high fullness ratio by oligo-capping, and [2] assembling 5'-end sequences and selecting one with the highest probability of completeness in length in the cluster formed (there are many clones longer in the 5'-end direction). However, the uses of primers designed based on the 5'- and 3'-end sequences of polynucleotides provided by the present invention enable readily obtaining full-length cDNAs without such a special technique. The primer, which is designed to be used for obtaining cDNAs capable of being expressed, is not limited to the 5'- and 3'-end sequences of polynucleotide.

[0016] Specifically, the present invention relates to a polynucleotide selected from the group consisting of the following (a) to (g):

(a) a polynucleotide comprising a protein-coding region of the nucleotide sequence of any one of SEQ ID NOs shown in Table 1;

(b) a polynucleotide encoding a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs shown in Table 1;

(c) a polynucleotide comprising a nucleotide sequence encoding a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs shown in Table 1, wherein, in said amino acid sequence, one or more amino

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acids have been substituted, deleted, inserted, and/or added, and wherein said nucleotide sequence encodes a polypeptide functionally equivalent to a polypeptide comprising the selected amino acid sequence;

(d) a polynucleotide hybridizing under stringent conditions to a polynucleotide comprising the nucleotide sequence of any one of SEQ ID NOs shown in Table 1, wherein said nucleotide sequence encodes a polypeptide functionally equivalent to a polypeptide encoded by the selected nucleotide sequence;

(e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a polypeptide encoded by the polynucleotide according to any one of (a) to (d);

(f) a polynucleotide comprising a nucleotide sequence having at least 70% identity to the nucleotide sequence of (a); and

(g) a polynucleotide comprising a nucleotide sequence having at least 90% identity to the nucleotide sequence of (a).

[0017] The present invention also relates to a polypeptide encoded by the above-mentioned polynucleotide or a partial peptide thereof, an antibody binding to the polypeptide or the peptide, and a method for immunologically assaying the polypeptide or the peptide, which comprises the steps of contacting the polypeptide or the peptide with the antibody and observing the binding between the two.

[0018] Furthermore, the present invention features a vector comprising the above-mentioned polynucleotide, a transformant carrying the polynucleotide or the vector, a transformant carrying the polynucleotide or the vector in an expressible manner, and a method for producing the polypeptide or the peptide, which comprises the steps of culturing the transformant and recovering an expression product.

[0019] Another feature of the present invention is an oligonucleotide comprising at least 15 nucleotides, said oligonucleotide comprising a nucleotide sequence complementary to the nucleotide sequence of any one of SEQ ID NOs: 1 to 1639 or to a complementary strand thereof. This oligonucleotide can be used as a primer for synthesizing the above-mentioned polynucleotide or used as a probe for detecting the polynucleotide. The present invention includes an antisense polynucleotide against the polynucleotide or a part thereof, and a method for detecting the polynucleotide, which comprises the following steps of:

- a) incubating a target polynucleotide with the oligonucleotide under hybridizable conditions, and
- b) detecting hybridization of the target polynucleotide with the oligonucleotide.

[0020] Still another feature of the present invention is a database of polynucleotides and/or polypeptides, said database comprising information on at least one of the nucleotide sequences of SEQ ID NOs: 1 to 1639 and/or on at least one of the amino acid sequences of SEQ ID NOs: 1640 to 3278.

[0021] Herein, "polynucleotide" is defined as a molecule, such as DNA and RNA, in which multiple nucleotides are polymerized. There are no limitations on the number of the polymerized nucleotides. In case that the polymer contains relatively low number of nucleotides, it is also described as an "oligonucleotide", which is included in the "polynucleotide" of the present invention. The polynucleotide or the oligonucleotide of the present invention can be a natural or chemically synthesized product. Alternatively, it can be synthesized using a template polynucleotide by an enzymatic reaction such as PCR. Furthermore, the polynucleotide of the present invention may be modified chemically. Moreover, not only a single-strand polynucleotide but also a double-strand polynucleotide is included in the present invention. In this specification, especially in claims, when the polynucleotide is described merely as "polynucleotide", it means not only a single-strand polynucleotide but also a double-strand polynucleotide. When it means double-strand polynucleotide, the nucleotide sequence of only one chain is indicated. However, based on the nucleotide sequence of a sense chain, the nucleotide sequence of the complementary strand thereof is essentially determined.

[0022] As used herein, an "isolated polynucleotide" is a polynucleotide the structure of which is not identical to that of any naturally occurring polynucleotide or to that of any fragment of a naturally occurring genomic polynucleotide spanning more than three separate genes. The term therefore includes, for example, (a) a DNA which has the sequence of part of a naturally occurring genomic DNA molecule in the genome of the organism in which it naturally occurs; (b) a polynucleotide incorporated into a vector or into the genomic DNA of a prokaryote or eukaryote in a manner such that the resulting molecule is not identical to any naturally occurring vector or genomic DNA; (c) a separate molecule such as a cDNA, a genomic fragment, a fragment produced by polymerase chain reaction (PCR), or a restriction fragment, and (d) a recombinant nucleotide sequence that is part of a hybrid gene, i.e., a gene encoding a fusion polypeptide. Specifically excluded from this definition are polynucleotides of DNA molecules present in mixtures of different (i) DNA molecules, (ii) transfected cells, or (iii) cell clones; e.g., as these occur in a DNA library such as a cDNA or genomic DNA library.

[0023] The term "substantially pure" as used herein in reference to a given protein or polypeptide means that the protein or polypeptide is substantially free from other biological macromolecules. For example, the substantially pure protein or polypeptide is at least 75%, 80%, 85%, 95%, or 99% pure by dry weight. Purity can be measured by any

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appropriate standard method known in the art, for example, by column chromatography, polyacrylamide gel electrophoresis, or HPLC analysis.

[0024] All the cDNAs provided by the present invention are full-length cDNAs. The "full-length cDNA" herein means that the cDNA contains the ATG codon, which is the start point of translation therein. The untranslated regions upstream and downstream of the protein-coding region, both of which are naturally contained in natural mRNAs, are not indispensable. It is preferable that the full-length cDNAs of the present invention contain the stop codon.

BRIEF DESCRIPTION OF THE DRAWINGS

[0025] Figure 1 shows the restriction map of the vector pME18SFL3.

DETAILED DESCRIPTION OF THE INVENTION

[0026] All the clones (1639 clones) of the present invention are novel and encode the full-length polypeptides. Further, all the clones are cDNAs with the high fullness ratio, which were obtained by oligo-capping method, and also clones which are not identical to any of known human mRNAs (namely, novel clones) selected by searching, for the 5'-end sequences, mRNA sequences with the annotation of "complete cds" in the GenBank and UniGene databases by using the BLAST homology search [S. F. Altschul, W. Gish, W. Miller, E. W. Myers & D. J. Lipman, J. Mol. Biol., 215: 403-410 (1990); W. Gish & D. J. States, Nature Genet., 3: 266-272 (1993)]; they are also clones that were assumed to have higher fullness ratio among the members in the cluster formed by assembling. Most of the clones assessed to have high fullness ratio in the cluster had the nucleotide sequences longer in the 5'-end direction.

[0027] All the full-length cDNAs of the present invention can be synthesized by a method such as PCR (Current protocols in Molecular Biology edit. Ausubel et al. (1987) Publish. John Wiley & Sons Section 6.1-6.4) using primer sets designed based on the 5'-end and 3'-end sequences or using primer sets of primers designed based on the 5'-end sequences and a primer of oligo dT sequence corresponding to poly A sequence. Table 1 contains the clone names of full-length cDNA of 1639 clones of the present invention, SEQ ID NOs of the full-length nucleotide sequences, CDS portions deduced from the full-length nucleotide sequences, and SEQ ID NOs of the translated amino acids. The positions of CDS are shown according to the rule of "DDBJ/EMBL/GenBank Feature Table Definition" (<http://www.ncbi.nlm.nih.gov/colab/FT/index.html>). The start position number corresponds to the first letter of "ATG" that is the nucleotide triplet encoding methionine; the termination position number corresponds to the third letter of the stop codon. These are indicated being flanked with the mark "...". However, with respect to the clones having no stop codon, the termination position is indicated by the mark ">" according to the above rule.

Table 1

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
3NB6910000180	1	505..1434	1640
3NB6910000850	2	132..836	1641
3NB6910001160	3	85..702	1642
3NB6910001290	4	194..706	1643
3NB6910001730	5	166..>1755	1644
3NB6920000290	6	991..1335	1645
3NB6920002810	7	8..1375	1646
3NB6920003300	8	128..901	1647
3NB6920005450	9	21..809	1648
3NB6920009120	10	247..1983	1649
3NB6920010020	11	59..913	1650
3NB6920010220	12	108..1289	1651
3NB6920013490	13	402..1214	1652
3NB6920014330	14	674..1516	1653
3NB6920014710	15	369..>1990	1654
3NB6920015110	16	306..1163	1655
3NB6920015280	17	162..1847	1656
3NB6920015570	18	407..1903	1657
3NB6920016370	19	25..348	1658

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	3NB6920017190	20	151..1068	1659
	ADRGL10000020	21	7..1773	1660
	ADRGL10000180	22	1742..2110	1661
	ADRGL10000850	23	425..1072	1662
10	ADRGL10001600	24	10..1407	1663
	ADRGL10001650	25	107..1387	1664
	ADRGL10001820	26	2165..2467	1665
	ADRGL20000740	27	114..1349	1666
15	ADRGL20003230	28	118..516	1667
	ADRGL20004280	29	169..477	1668
	ASTR010000180	30	158..2716	1669
	ASTR020000950	31	110..1315	1670
20	ASTR020004170	32	1121..1732	1671
	ASTR020004800	33	1177..1539	1672
	BGGI110002850	34	1119..1460	1673
	BGGI120001610	35	454..1185	1674
25	BGGI120005330	36	79..1548	1675
	BGGI120005440	37	453..1661	1676
	BGGI120006840	38	140..1303	1677
	BGGI120006930	39	38..1627	1678
30	BGGI120010970	40	264..2078	1679
	BGGI120017140	41	140..1009	1680
	BNGH410000030	42	780..1967	1681
	BNGH410000130	43	1087..1539	1682
35	BNGH410000170	44	1466..1801	1683
	BNGH410000290	45	51..1661	1684
	BNGH410000330	46	2453..2782	1685
	BNGH410000340	47	539..1477	1686
40	BNGH410000390	48	134..1135	1687
	BNGH410000800	49	232..549	1688
	BNGH410001040	50	146..1651	1689
	BNGH410001180	51	166..>2624	1690
45	BNGH410001370	52	61..1740	1691
	BNGH410001530	53	1368..1760	1692
	BNGH410001770	54	82..1773	1693
	BNGH410001900	55	113..>2458	1694
50	BNGH410001980	56	97..1476	1695
	BNGH420004740	57	1171..1473	1696
	BNGH420005320	58	354..1937	1697
	BRACE10000200	59	959..1267	1698
55	BRACE10000420	60	214..1332	1699
	BRACE10000700	61	181..900	1700
	BRACE10000730	62	168..698	1701
	BRACE10000930	63	45..1388	1702
60	BRACE10001150	64	76..624	1703
	BRACE10001590	65	225..767	1704
	BRACE10001660	66	777..1325	1705
	BRACE10001690	67	557..889	1706
65	BRACE10001870	68	85..1704	1707

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	BRACE20000770	69	162..605	1708
	BRACE20001000	70	1122..1430	1709
	BRACE20001410	71	229..975	1710
	BRACE20002800	72	35..1663	1711
10	BRACE20003320	73	471..2063	1712
	BRACE20004210	74	1562..2716	1713
	BRACE20005050	75	711..1013	1714
	BRACE20005250	76	617..1144	1715
15	BRACE20005450	77	184..498	1716
	BRACE20005650	78	272..841	1717
	BRACE20005770	79	514..816	1718
	BRACE20006980	80	85..1446	1719
20	BRACE20007180	81	1263..1679	1720
	BRACE20008850	82	596..>1809	1721
	BRACE20009880	83	1761..2069	1722
	BRACE20010650	84	1257..1922	1723
25	BRACE20010700	85	1680..>1989	1724
	BRACE20011170	86	87..410	1725
	BRACE20011430	87	1550..2041	1726
	BRACE20011880	88	742..1104	1727
30	BRACE20013400	89	1495..1890	1728
	BRACE20013520	90	677..1048	1729
	BRACE20013740	91	1694..2317	1730
	BRACE20013750	92	821..1192	1731
35	BRACE20014230	93	1523..1978	1732
	BRACE20014530	94	1747..2205	1733
	BRACE20014550	95	921..1838	1734
	BRACE20014770	96	351..1286	1735
40	BRACE20014920	97	1306..1638	1736
	BRACE20015080	98	39..545	1737
	BRACE20015430	99	235..579	1738
	BRACE20016730	100	445..828	1739
45	BRACE20016920	101	96..569	1740
	BRACE20017370	102	1612..2082	1741
	BRACE20018550	103	152..2008	1742
	BRACE20018590	104	902..1408	1743
50	BRACE20018650	105	1143..1529	1744
	BRACE20018980	106	2178..2558	1745
	BRACE20019440	107	225..1205	1746
	BRACE20020500	108	605..1372	1747
55	BRACE20020910	109	283..1176	1748
	BRACE20021510	110	1003..1653	1749
	BRACE20021760	111	393..1148	1750
	BRACE20022020	112	717..1727	1751
55	BRACE20022270	113	3..353	1752
	BRACE20024090	114	165..845	1753
	BRACE20024310	115	2292..2618	1754
	BRACE20024680	116	65..1129	1755
	BRACE20024780	117	297..1154	1756

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	BRACE20024950	118	49..369	1757
	BRACE20025900	119	636..941	1758
	BRACE20026350	120	106..753	1759
	BRACE20026850	121	113..1063	1760
	BRACE20027360	122	1147..1680	1761
10	BRACE20027520	123	613..1215	1762
	BRACE20027550	124	168..578	1763
	BRACE20027720	125	169..777	1764
	BRACE20027920	126	105..1496	1765
15	BRACE20027960	127	1731..2132	1766
	BRACE20028120	128	408..917	1767
	BRACE20028600	129	784..1593	1768
	BRACE20028610	130	774..1196	1769
	BRACE20028960	131	63..1472	1770
20	BRACE20030780	132	236..637	1771
	BRACE20031100	133	214..2565	1772
	BRACE20032850	134	698..1327	1773
	BRACE20033190	135	202..531	1774
25	BRACE20033980	136	811..1215	1775
	BRACE20034310	137	526..1461	1776
	BRACE20034490	138	1316..1699	1777
	BRACE20035160	139	492..896	1778
	BRACE20035270	140	572..1099	1779
30	BRACE20035390	141	891..1211	1780
	BRACE20035940	142	80..601	1781
	BRACE20071380	143	190..1335	1782
	BRACE20071530	144	62..604	1783
35	BRACE20071740	145	118..1800	1784
	BRACE20071970	146	1584..1895	1785
	BRACE20072010	147	422..1114	1786
	BRACE20072320	148	266..583	1787
	BRACE20072810	149	858..1193	1788
40	BRACE20074010	150	92..1246	1789
	BRACE20074470	151	742..2109	1790
	BRACE20075020	152	2248..2553	1791
	BRACE20075270	153	1740..2285	1792
45	BRACE20075380	154	1455..1889	1793
	BRACE20075630	155	996..1445	1794
	BRACE20076210	156	850..1509	1795
	BRACE20076410	157	78..1040	1796
	BRACE20076460	158	1368..1709	1797
50	BRACE20076630	159	634..996	1798
	BRACE20076850	160	598..984	1799
	BRACE20077080	161	119..853	1800
	BRACE20077270	162	95..445	1801
	BRACE20077610	163	239..553	1802
55	BRACE20077640	164	595..900	1803
	BRACE20077670	165	317..649	1804
	BRACE20077680	166	2013..2390	1805

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	BRACE20077840	167	18..524	1806
	BRACE20077980	168	855..1604	1807
	BRACE20078680	169	1144..>1753	1808
	BRACE20078820	170	2..580	1809
	BRACE20079020	171	1178..1681	1810
10	BRACE20079530	172	8..331	1811
	BRACE20080970	173	1025..1348	1812
	BRACE20081140	174	14..463	1813
	BRACE20083800	175	71..1201	1814
	BRACE20083850	176	183..1046	1815
15	BRACE20084430	177	1035..1649	1816
	BRACE20084800	178	57..845	1817
	BRACE20084880	179	1234..1617	1818
	BRACE20086530	180	405..914	1819
	BRACE20086550	181	219..632	1820
20	BRACE20087080	182	31..342	1821
	BRACE20087540	183	1013..1459	1822
	BRACE20088570	184	42..365	1823
	BRACE20089600	185	121..630	1824
	BRACE20089990	186	446..928	1825
25	BRACE20090140	187	677..979	1826
	BRACE20091880	188	18..539	1827
	BRACE20092120	189	160..1959	1828
	BRACE20092740	190	255..905	1829
	BRACE20092750	191	1450..1827	1830
30	BRACE20093070	192	562..1158	1831
	BRACE20093110	193	1581..1940	1832
	BRACE20093610	194	1337..>1783	1833
	BRACE20094370	195	826..1149	1834
	BRACE20095170	196	1657..1959	1835
35	BRAWH10000010	197	1241..2050	1836
	BRAWH10000020	198	869..>1920	1837
	BRAWH10000070	199	560..2242	1838
	BRAWH10000370	200	161..787	1839
	BRAWH10000940	201	203..2020	1840
40	BRAWH10001300	202	256..2025	1841
	BRAWH10001620	203	109..1128	1842
	BRAWH10001640	204	185..613	1843
	BRAWH10001680	205	229..987	1844
	BRAWH10001740	206	277..1383	1845
45	BRAWH10001800	207	182..601	1846
	BRAWH20000340	208	2214..2537	1847
	BRAWH20000480	209	218..1117	1848
	BRAWH20000930	210	1521..1904	1849
	BRAWH20001090	211	356..2014	1850
50	BRAWH20001770	212	69..476	1851
	BRAWH20002480	213	1385..1777	1852
	BRAWH20003230	214	232..780	1853
	BRAWH20004430	215	222..2186	1854

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	BRAWH20004760	216	22..564	1855
	BRAWH20005030	217	1431..1754	1856
	BRAWH20005220	218	98..700	1857
	BRAWH20005540	219	416..811	1858
10	BRAWH20006330	220	854..1741	1859
	BRAWH20006510	221	438..1163	1860
	BRAWH20006860	222	599..2179	1861
	BRAWH20006970	223	1178..1579	1862
15	BRAWH20008660	224	505..924	1863
	BRAWH20008920	225	2179..2529	1864
	BRAWH20009010	226	1139..1540	1865
	BRAWH20009440	227	422..1603	1866
20	BRAWH20009840	228	826..1764	1867
	BRAWH20011030	229	1881..2186	1868
	BRAWH20011290	230	71..1444	1869
	BRAWH20011410	231	251..718	1870
25	BRAWH20011660	232	104..1411	1871
	BRAWH20012030	233	55..684	1872
	BRAWH20014180	234	5..751	1873
	BRAWH20014380	235	795..1130	1874
30	BRAWH20014610	236	743..1216	1875
	BRAWH20014840	237	404..2227	1876
	BRAWH20015030	238	861..1232	1877
	BRAWH20036890	239	319..864	1878
35	BRAWH20036930	240	28..3078	1879
	BRAWH20038320	241	998..1306	1880
	BRAWH20040950	242	1867..2205	1881
	BRAWH20047310	243	47..547	1882
40	BRAWH20052250	244	30..398	1883
	BRAWH20059980	245	161..1900	1884
	BRAWH20060440	246	65..2083	1885
	BRAWH20064500	247	209..1675	1886
45	BRAWH20064930	248	403..1908	1887
	BRAWH20066220	249	1395..>2080	1888
	BRAWH20069600	250	1482..1976	1889
	BRAWH20069890	251	444..1226	1890
50	BRAWH20074060	252	1028..1429	1891
	BRAWH20076050	253	45..1469	1892
	BRAWH20087060	254	1160..2053	1893
	BRAWH20089030	255	346..825	1894
55	BRAWH20089560	256	87..2906	1895
	BRAWH20092270	257	223..1062	1896
	BRAWH20092610	258	258..791	1897
	BRAWH20093600	259	21..644	1898
55	BRAWH20094850	260	1213..1536	1899
	CD34C20000510	261	7..1380	1900
	CTONG20003030	262	2228..2641	1901
	CTONG20005890	263	294..3017	1902
	CTONG20007710	264	1088..1468	1903

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	CTONG20008270	265	863..2080	1904
	CTONG20011390	266	50..3337	1905
	CTONG20013200	267	123..1823 1823	1906
	CTONG20013660	268	3..1571	1907
10	CTONG20015330	269	87..527	1908
	CTONG20018200	270	42..>3217	1909
	CTONG20019110	271	511..1455	1910
	CTONG20019550	272	162..>3684	1911
15	CTONG20020730	273	20..1342	1912
	CTONG20021430	274	74..>2745	1913
	CTONG20024180	275	641..2452	1914
	CTONG20024530	276	618..986	1915
20	CTONG20025580	277	1281..2177	1916
	CTONG20027210	278	366..>2763	1917
	CTONG20028030	279	837..1280	1918
	CTONG20028160	280	301..2799	1919
25	CTONG20028200	281	148..>3543	1920
	CTONG20029650	282	118..>2551	1921
	CTONG20037820	283	332..895	1922
	CTONG20047160	284	113..1021	1923
30	CTONG20055530	285	63..>2305	1924
	CTONG20064490	286	1533..1859	1925
	D30ST20001840	287	77..1429	1926
	DFNES20002120	288	1263..1940	1927
35	DFNES20002680	289	505..2571	1928
	DFNES20002920	290	52..639	1929
	DFNES20003350	291	33..1007	1930
	DFNES20004320	292	1517..1849	1931
40	FCBBF10005980	293	375..2141	1932
	FCBBF10006180	294	1161..1463	1933
	FCBBF10006750	295	106..1023	1934
	FCBBF10006880	296	521..865	1935
45	FCBBF10006870	297	410..1831	1936
	FCBBF10006910	298	111..482	1937
	FCBBF10007320	299	1236..1850	1938
	FCBBF10007600	300	68..523	1939
50	FCBBF20000940	301	249..2147	1940
	FCBBF20001050	302	29..421	1941
	FCBBF20001950	303	1565..1888	1942
	FCBBF20002320	304	921..2003	1943
55	FCBBF20002760	305	221..895	1944
	FCBBF20005780	306	693..1073	1945
	FCBBF20005910	307	29..>2161	1946
	FCBBF20006770	308	265..600	1947
60	FCBBF20007330	309	745..1077	1948
	FCBBF20008080	310	180..821	1949
	FCBBF20008150	311	641..1762	1950
	FCBBF20009400	312	360..749	1951
	FCBBF20009510	313	218..1333	1952

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	FCBBF20012110	314	136..1776	1953
	FCBBF20012990	315	758..1168	1954
	FCBBF20014800	316	146..1957	1955
	FCBBF20015380	317	302..1246	1956
	FCBBF20016720	318	51..488	1957
10	FCBBF20017180	319	236..598	1958
	FCBBF20017200	320	2306..2767	1959
	FCBBF40002820	321	207..1247	1960
	FCBBF50002610	322	126..1634	1961
	FEBRA20000350	323	724..1764	1962
15	FEBRA20000530	324	359..2221	1963
	FEBRA20001050	325	496..2355	1964
	FEBRA20001290	326	872..1192	1965
	FEBRA20003110	327	386..964	1966
	FEBRA20003300	328	1504..1881	1967
20	FEBRA20003770	329	398..2464	1968
	FEBRA20003780	330	454..873	1969
	FEBRA20003910	331	1728..2057	1970
	FEBRA20003970	332	162..1469	1971
	FEBRA20003990	333	845..2404	1972
25	FEBRA20004040	334	21..449	1973
	FEBRA20004150	335	836..2494	1974
	FEBRA20004520	336	113..442	1975
	FEBRA20004540	337	934..2484	1976
	FEBRA20004910	338	1417..1926	1977
30	FEBRA20005360	339	254..1453	1978
	FEBRA20006560	340	34..615	1979
	FEBRA20006800	341	303..1040	1980
	FEBRA20006900	342	1268..1669	1981
	FEBRA20007330	343	1486..2013	1982
35	FEBRA20007400	344	32..1123	1983
	FEBRA20007570	345	222..1193	1984
	FEBRA20007710	346	1059..1361	1985
	FEBRA20007720	347	267..689	1986
	FEBRA20007870	348	1174..1788	1987
40	FEBRA20008090	349	1319..1621	1988
	FEBRA20008560	350	1500..1991	1989
	FEBRA20008740	351	2051..2368	1990
	FEBRA20008800	352	38..703	1991
	FEBRA20008810	353	377..1495	1992
45	FEBRA20009010	354	243..638	1993
	FEBRA20009590	355	1345..1677	1994
	FEBRA20009720	356	530..2140	1995
	FEBRA20010930	357	239..1249	1996
	FEBRA20011330	358	1795..2322	1997
50	FEBRA20011460	359	2219..2602	1998
	FEBRA20011970	360	1672..1977	1999
	FEBRA20012270	361	1933..2238	2000
	FEBRA20012450	362	519..2678	2001

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	FEBRA20012940	363	69..575	2002
	FEBRA20013510	364	990..1313	2003
	FEBRA20014870	365	1567..1884	2004
	FEBRA20014920	366	77..2815	2005
10	FEBRA20015840	367	702..1853	2006
	FEBRA20015900	368	1535..1882	2007
	FEBRA20015910	369	246..617	2008
	FEBRA20017060	370	730..1257	2009
15	FEBRA20017150	371	391..2799	2010
	FEBRA20017900	372	72..647	2011
	FEBRA20019890	373	497..2239	2012
	FEBRA20020860	374	281..673	2013
20	FEBRA20021910	375	1455..1829	2014
	FEBRA20021940	376	17..493	2015
	FEBRA20024290	377	35..1933	2016
	FEBRA20024420	378	991..1614	2017
25	FEBRA20025250	379	251..2164	2018
	FEBRA20027270	380	10..930	2019
	FEBRA20027830	381	293..610	2020
	FEBRA20028820	382	1337..1678	2021
30	FEBRA20028970	383	824..1303	2022
	FEBRA20029080	384	90..764	2023
	FEBRA20030540	385	292..993	2024
	FEBRA20031550	386	2000..2365	2025
35	FEBRA20033080	387	399..749	2026
	FEBRA20034290	388	348..854	2027
	FEBRA20037070	389	1830..>2246	2028
	FEBRA20041100	390	198..1010	2029
40	FEBRA20041910	391	39..425	2030
	FEBRA20042240	392	1373..1714	2031
	FEBRA20042370	393	51..938	2032
	FEBRA20042930	394	2321..>2652	2033
45	FEBRA20043250	395	394..>2294	2034
	FEBRA20043290	396	57..2984	2035
	FEBRA20044120	397	928..1263	2036
	FEBRA20044430	398	192..539	2037
50	FEBRA20044900	399	78..1763	2038
	FEBRA20045920	400	344..1438	2039
	FEBRA20048180	401	86..493	2040
	FEBRA20050140	402	727..2325	2041
55	FEBRA20050790	403	780..1295	2042
	FEBRA20052160	404	1055..1411	2043
	FEBRA20053770	405	790..1197	2044
	FEBRA20053800	406	213..521	2045
	FEBRA20054270	407	1711..2058	2046
	FEBRA20057260	408	8..1789	2047
	FEBRA20057520	409	13..480	2048
	FEBRA20057780	410	150..641	2049
	FEBRA20057880	411	8..>3165	2050

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	FEBRA20059380	412	1160..2017	2051
	FEBRA20060920	413	26..661	2052
	FEBRA20061500	414	77..460	2053
	FEBRA20062700	415	32..778	2054
10	FEBRA20063150	416	236..538	2055
	FEBRA20063540	417	1402..1737	2056
	FEBRA20064760	418	340..2076	2057
	FEBRA20066270	419	278..691	2058
15	FEBRA20066670	420	1933..2496	2059
	FEBRA20067360	421	160..1713	2060
	FEBRA20067930	422	1332..1973	2061
	FEBRA20068730	423	171..2051	2062
20	FEBRA20069420	424	231..1439	2063
	FEBRA20070170	425	88..921	2064
	FEBRA20072000	426	47..2065	2065
	FEBRA20072800	427	1850..2335	2066
25	FEBRA20074140	428	57..371	2067
	FEBRA20074580	429	91..420	2068
	FEBRA20075510	430	181..606	2069
	FEBRA20075660	431	1960..2298	2070
30	FEBRA20078220	432	147..2525	2071
	HCASM10000210	433	384..1154	2072
	HCASM10000610	434	317..871	2073
	HCASM10001150	435	473..868	2074
35	HCASM20002020	436	152..469	2075
	HCASM20002140	437	408..1136	2076
	HCASM20003070	438	48..1865	2077
	HCASM20005340	439	1003..1368	2078
40	HCASM20005360	440	2211..2618	2079
	HEART20000350	441	514..1290	2080
	HEART20000990	442	1341..1670	2081
	HEART20003090	443	1133..1657	2082
45	HEART20004110	444	39..1415	2083
	HEART20004480	445	863..1171	2084
	HEART20004920	446	159..851	2085
	HEART20005060	447	95..1495	2086
50	HEART20005200	448	938..1375	2087
	HEART20005680	449	783..1139	2088
	HHDP20000550	450	55..1320	2089
	HHDP20000950	451	338..1462	2090
55	HHDP20001150	452	326..925	2091
	HHDP20001490	453	337..2265	2092
	HHDP20003150	454	506..1711	2093
	HHDP20004550	455	197..2065	2094
55	HHDP20004560	456	174..>2424	2095
	HHDP20004620	457	17..865	2096
	HLUNG10000240	458	1439..1762	2097
	HLUNG10000300	459	205..555	2098
	HLUNG10000370	460	14..1930	2099

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	HLUNG10000640	461	144..1514	2100
	HLUNG10000760	462	80..1246	2101
	HLUNG10000990	463	67..2370	2102
	HLUNG10001050	464	1081..1614	2103
	HLUNG10001100	465	302..703	2104
10	HLUNG20000680	466	187..1527	2105
	HLUNG20001160	467	391..1434	2106
	HLUNG20001250	468	360..899	2107
	HLUNG20001420	469	173..1600	2108
	HLUNG20001760	470	6..524	2109
15	HLUNG20002550	471	1101..1865	2110
	HLUNG20003140	472	36..359	2111
	HLUNG20004120	473	416..820	2112
	HLUNG20004800	474	1400..1711	2113
	HLUNG20005010	475	37..966	2114
20	HSYRA10001190	476	159..1712	2115
	HSYRA10001370	477	194..1903	2116
	HSYRA10001480	478	27..614	2117
	HSYRA10001680	479	59..>2245	2118
	HSYRA10001780	480	598..1023	2119
25	HSYRA20001350	481	218..2371	2120
	HSYRA20002480	482	670..972	2121
	HSYRA20002530	483	214..780	2122
	HSYRA20003470	484	1134..1580	2123
	HSYRA20005100	485	138..1379	2124
30	HSYRA20006050	486	66..1199	2125
	HSYRA20006290	487	222..1160	2126
	HSYRA20006400	488	648..1052	2127
	HSYRA20007600	489	389..1207	2128
	HSYRA20008280	490	1492..1821	2129
35	HSYRA20011030	491	572..>2236	2130
	HSYRA20011530	492	653..955	2131
	HSYRA20013320	493	3..956	2132
	HSYRA20014200	494	326..1237	2133
	HSYRA20014760	495	46..783	2134
40	HSYRA20015740	496	117..947	2135
	HSYRA20015800	497	1100..1435	2136
	HSYRA20016210	498	81..470	2137
	HSYRA20016310	499	317..1105	2138
	IMR3210000440	500	313..1560	2139
50	IMR3210000740	501	1215..1616	2140
	IMR3210000750	502	722..1054	2141
	IMR3210001580	503	125..1249	2142
	IMR3210001650	504	903..1391	2143
	IMR3210002420	505	194..1255	2144
55	IMR3210002660	506	38..1423	2145
	IMR3220002230	507	25..945	2146
	IMR3220003020	508	403..1425	2147
	IMR3220006090	509	8..442	2148

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	IMR3220007420	510	15..614	2149
	IMR3220007760	511	197..>1670	2150
	IMR3220007910	512	934..1515	2151
	IMR3220008380	513	228..1142	2152
10	IMR3220008590	514	756..1061	2153
	IMR3220008630	515	94..1197	2154
	IMR3220009190	516	31..1293	2155
	IMR3220009350	517	20..421	2156
15	IMR3220009530	518	2..394	2157
	IMR3220009730	519	102..>2141	2158
	IMR3220009840	520	246..554	2159
	IMR3220011850	521	271..1026	2160
20	IMR3220012180	522	76..1521	2161
	IMR3220013170	523	393..1028	2162
	IMR3220013320	524	22..1140	2163
	IMR3220014350	525	807..2027	2164
25	IMR3220014910	526	79..639	2165
	IMR3220016000	527	8..532	2166
	IMR3220017240	528	1114..1458	2167
	KIDNE10000080	529	346..1233	2168
30	KIDNE10000280	530	1864..2181	2169
	KIDNE10000500	531	662..1108	2170
	KIDNE10001040	532	115..1656	2171
	KIDNE10001430	533	560..1051	2172
35	KIDNE10001460	534	7..483	2173
	KIDNE10001520	535	74..712	2174
	KIDNE20000410	536	712..1215	2175
	KIDNE20000510	537	188..1717	2176
40	KIDNE20000700	538	843..2135	2177
	KIDNE20000850	539	19..1071	2178
	KIDNE20001670	540	727..1725	2179
	KIDNE20001920	541	1648..2070	2180
45	KIDNE20002440	542	163..468	2181
	KIDNE20002450	543	1273..1653	2182
	KIDNE20002660	544	1929..2249	2183
	KIDNE20003150	545	926..1306	2184
50	KIDNE20003300	546	1205..2230	2185
	KIDNE20003490	547	219..1523	2186
	KIDNE20003750	548	732..1568	2187
	KIDNE20004030	549	194..3142	2188
55	KIDNE20004220	550	1699..2217	2189
	KIDNE20004970	551	274..1479	2190
	KIDNE20005130	552	404..1417	2191
	KIDNE20005170	553	57..944	2192
	KIDNE20005190	554	530..1045	2193
	KIDNE20005740	555	32..1309	2194
	KIDNE2003185	556	1050..>1998	2195
	KIDNE20033050	557	121..1719	2196
	KIDNE20033350	558	1999..2304	2197

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	KIDNE20033570	559	269..634	2198
	KIDNE20033730	560	408..2366	2199
	KIDNE20033770	561	1256..1603	2200
	KIDNE20037520	562	1032..1637	2201
10	KIDNE20039410	563	263..928	2202
	KIDNE20039940	564	133..1134	2203
	KIDNE20040340	565	460..768	2204
	KIDNE20040540	566	5..1276	2205
15	KIDNE20040840	567	5...3343	2206
	KIDNE20042620	568	1312..1716	2207
	KIDNE20042940	569	213..611	2208
	KIDNE20042950	570	72..476	2209
20	KIDNE20043440	571	49..2136	2210
	KIDNE20044110	572	167..1708	2211
	KIDNE20045200	573	1455..1955	2212
	KIDNE20045340	574	44..919	2213
25	KIDNE20045790	575	1561..2085	2214
	KIDNE20046810	576	398..1066	2215
	KIDNE20048280	577	124..2010	2216
	KIDNE20048640	578	1437..1775	2217
30	KIDNE20048790	579	348..701	2218
	KIDNE20049810	580	909..2108	2219
	KIDNE20050420	581	183..2351	2220
	KIDNE20052960	582	1105..1461	2221
35	KIDNE20053360	583	1054..1470	2222
	KIDNE20054000	584	1246..1596	2223
	KIDNE20054770	585	99..1511	2224
	KIDNE20056290	586	398..1306	2225
40	KIDNE20056760	587	375..1493	2226
	KIDNE20059080	588	44..>2546	2227
	KIDNE20059370	589	1683..2018	2228
	KIDNE20060140	590	52..1572	2229
45	KIDNE20060300	591	42..530	2230
	KIDNE20060530	592	136..2208	2231
	KIDNE20060620	593	31..687	2232
	KIDNE20061490	594	824..1327	2233
50	KIDNE20062480	595	649..963	2234
	KIDNE20062990	596	72..1334	2235
	KIDNE20063530	597	710..1105	2236
	KIDNE20063760	598	1332..1724	2237
55	KIDNE20066520	599	112..435	2238
	KIDNE20067600	600	677..1795	2239
	KIDNE20067750	601	54..2228	2240
	KIDNE20068800	602	1048..1473	2241
55	KIDNE20070050	603	1672..2001	2242
	KIDNE20070770	604	610..1845	2243
	KIDNE20071860	605	1662..1973	2244
	KIDNE20073280	606	24..1898	2245
	KIDNE20073520	607	332..2140	2246

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	KIDNE20073560	608	171..497	2247
	KIDNE20074220	609	1496..1879	2248
	KIDNE20075690	610	231..911	2249
	KIDNE20078100	611	714..1373	2250
	KIDNE20078110	612	166..1482	2251
10	LIVER10000580	613	1704..2108	2252
	LIVER10000670	614	33..2063	2253
	LIVER10000790	615	98..1072	2254
	LIVER10000990	616	1451..2065	2255
15	LIVER10001040	617	710..1759	2256
	LIVER10001110	618	549..878	2257
	LIVER10001750	619	1737..2156	2258
	LIVER10002300	620	861..1565	2259
	LIVER10002780	621	2235..2699	2260
20	LIVER10003030	622	2310..2621	2261
	LIVER10004330	623	22..2130	2262
	LIVER10005420	624	131..2035	2263
	LIVER20000330	625	135..839	2264
25	LIVER20000370	626	1158..2138	2265
	LIVER20004160	627	1625..1966	2266
	LIVER20004460	628	882..1307	2267
	LIVER20005150	629	1453..2262	2268
	MAMGL10000320	630	71..1792	2269
30	MAMGL10000350	631	307..2721	2270
	MAMGL10000560	632	78..623	2271
	MAMGL10001780	633	1019..1618	2272
	MAMGL10001820	634	92..1405	2273
35	MAMGL10001840	635	636..1181	2274
	MESAN10000350	636	362..1843	2275
	MESAN10001010	637	54..2279	2276
	MESAN10001470	638	1571..1906	2277
	MESAN10001800	639	482..1900	2278
40	MESAN20000920	640	546..2213	2279
	MESAN20001490	641	652..>2706	2280
	MESAN20002670	642	1092..1535	2281
	MESAN20002910	643	1625..2269	2282
45	MESAN20003370	644	198..521	2283
	MESAN20005010	645	183..1550	2284
	NB9N410000470	646	329..>1714	2285
	NB9N410001210	647	74..1786	2286
	NB9N410001350	648	194..619	2287
50	NB9N410001460	649	678..1136	2288
	NB9N420000420	650	596..928	2289
	NB9N420001040	651	12..2030	2290
	NB9N420004950	652	1929..2648	2291
55	NESOP10000870	653	793..1554	2292
	NHNPC10000840	654	720..>1934	2293
	NHNPC10001010	655	119..541	2294
	NHNPC10001240	656	1513..1860	2295

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	NHNPC20002060	657	113..1351	2296
	NHNPC20002120	658	98..1195	2297
	NT2NE10000940	659	274..618	2298
	NT2NE10000140	660	232..>2244	2299
10	NT2NE10000180	661	131..1189	2300
	NT2NE10000230	662	172..483	2301
	NT2NE10000630	663	175..1317	2302
	NT2NE10000730	664	585..1364	2303
15	NT2NE10000830	665	556..1179	2304
	NT2NE10001200	666	431..874	2305
	NT2NE10001630	667	600..1013	2306
	NT2NE10001850	668	23..1960	2307
20	NT2NE20000380	669	408..962	2308
	NT2NE20000560	670	93..>1858	2309
	NT2NE20000640	671	731..1063	2310
	NT2NE20001740	672	1..1638	2311
25	NT2NE20002140	673	56..2053	2312
	NT2NE20002590	674	233..961	2313
	NT2NE20002990	675	117..1565	2314
	NT2NE20003270	676	127..>2256	2315
30	NT2NE20003690	677	534..893	2316
	NT2NE20003840	678	91..2403	2317
	NT2NE20003920	679	372..749	2318
	NT2NE20004550	680	31..852	2319
35	NT2NE20004700	681	1569..2048	2320
	NT2NE20005170	682	217..990	2321
	NT2NE20005360	683	1412..1717	2322
	NT2NE20005500	684	574..1605	2323
40	NT2NE20005860	685	289..996	2324
	NT2NE20006360	686	1383..>2954	2325
	NT2NE20006580	687	937..2073	2326
	NT2NE20007060	688	640..1053	2327
45	NT2NE20007630	689	11..679	2328
	NT2NE20007870	690	508..1092	2329
	NT2NE20008020	691	420..776	2330
	NT2NE20008090	692	328..1995	2331
50	NT2NE20009800	693	547..1164	2332
	NT2NE20011560	694	78..1037	2333
	NT2NE20012470	695	204..614	2334
	NT2NE20013240	696	747..1079	2335
55	NT2NE20013370	697	1229..2533	2336
	NT2NE20013640	698	1854..2264	2337
	NT2NE20013720	699	159..695	2338
	NT2NE20014030	700	1466..2263	2339
	NT2NE20014280	701	439..903	2340
	NT2NE20014350	702	684..1190	2341
	NT2NE20015300	703	120..>2517	2342
	NT2NE20016230	704	713..1111	2343
	NT2NE20016260	705	528..1721	2344

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	NT2NE20016340	706	575..1945	2345
	NT2NE20016480	707	5..388	2346
	NT2NE20016860	708	349..918	2347
	NT2NE20016970	709	48..566	2348
	NT2NE20034080	710	119..1606	2349
10	NT2NE20035690	711	969..>2204	2350
	NT2NE20044900	712	431..1039	2351
	NT2NE20047160	713	658..1707	2352
	NT2NE20053710	714	406..1020	2353
	NT2NE20054410	715	975..1715	2354
15	NT2NE20055170	716	50..955	2355
	NT2NE20057200	717	205..879	2356
	NT2RI10000160	718	290..1270	2357
	NT2RI10000270	719	330..809	2358
	NT2RI10000480	720	502..1068	2359
20	NT2RI10001640	721	4..>2060	2360
	NT2RI20000640	722	1391..1894	2361
	NT2RI20002700	723	849..1253	2362
	NT2RI20002820	724	195..1781	2363
	NT2RI20002940	725	63..467	2364
25	NT2RI20003410	726	148..1878	2365
	NT2RI20004120	727	23..1600	2366
	NT2RI20004210	728	477..1367	2367
	NT2RI20005970	729	309..1562	2368
	NT2RI20006690	730	206..>2507	2369
30	NT2RI20006710	731	884..1654	2370
	NT2RI20006850	732	550..2235	2371
	NT2RI20007380	733	843..1208	2372
	NT2RI20008650	734	692..1045	2373
	NT2RI20009740	735	287..595	2374
35	NT2RI20010100	736	150..1727	2375
	NT2RI20010830	737	295..2325	2376
	NT2RI20010910	738	361..1254	2377
	NT2RI20012350	739	969..1331	2378
	NT2RI20012440	740	1026..1367	2379
40	NT2RI20013420	741	6..506	2380
	NT2RI20013850	742	838..1497	2381
	NT2RI20014090	743	57..1739	2382
	NT2RI20014100	744	1280..1612	2383
	NT2RI20014490	745	244..2247	2384
45	NT2RI20014500	746	451..2331	2385
	NT2RI20015190	747	388..1671	2386
	NT2RI20015400	748	454..2277	2387
	NT2RI20015950	749	575..1078	2388
	NT2RI20016210	750	571..1113	2389
50	NT2RI20016570	751	238..1026	2390
	NT2RI20017260	752	1143..1703	2391
	NT2RI20018460	753	64..>2603	2392
	NT2RI20018660	754	245..1672	2393

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	NT2R120020220	755	571..1485	2394
	NT2R120020410	756	398..850	2395
	NT2R120021520	757	505..1482	2396
	NT2R120022430	758	1..1350	2397
10	NT2R120022520	759	1165..1629	2398
	NT2R120022700	760	532..1401	2399
	NT2R120025170	761	90..1727	2400
	NT2R120025300	762	570...>2759	2401
15	NT2R120025410	763	15..1757	2402
	NT2R120025540	764	170...>2080	2403
	NT2R120025850	765	245..1816	2404
	NT2R120028540	766	191..1555	2405
20	NT2R120028020	767	1..420	2406
	NT2R120028520	768	120..692	2407
	NT2R120029260	769	1253..1714	2408
	NT2R120029580	770	350..2023	2409
25	NT2R120029700	771	312..881	2410
	NT2R120030110	772	248..862	2411
	NT2R120030190	773	43..357	2412
	NT2R120030510	774	1317..1715	2413
30	NT2R120030670	775	714..1046	2414
	NT2R120031540	776	84..1538	2415
	NT2R120032050	777	698..2797	2416
	NT2R120032220	778	640...>2800	2417
35	NT2R120033010	779	652..2898	2418
	NT2R120033040	780	408..794	2419
	NT2R120033380	781	121..1374	2420
	NT2R120033440	782	650..1687	2421
40	NT2R120033830	783	165..929	2422
	NT2R120035560	784	27..1883	2423
	NT2R120036780	785	513..2585	2424
	NT2R120036950	786	355..2445	2425
45	NT2R120037510	787	591..1589	2426
	NT2R120040590	788	605..1597	2427
	NT2R120041900	789	86..442	2428
	NT2R120042840	790	760..1083	2429
50	NT2R120043040	791	236..1867	2430
	NT2R120043980	792	76..549	2431
	NT2R120044420	793	1080..1454	2432
	NT2R120046060	794	782..1480	2433
55	NT2R120047830	795	297..623	2434
	NT2R120048400	796	16..324	2435
	NT2R120049160	797	668..1054	2436
	NT2R120049840	798	1266..2060	2437
60	NT2R120049850	799	783..1973	2438
	NT2R120050610	800	19..2301	2439
	NT2R120050870	801	101..2056	2440
	NT2R120051500	802	236..1246	2441
	NT2R120053350	803	128..2125	2442

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	NT2R120053680	804	310..>2430	2443
	NT2R120055640	805	68..1171	2444
	NT2R120056280	806	1493..1954	2445
	NT2R120056470	807	272..2098	2446
	NT2R120057230	808	118..>1116	2447
10	NT2R120058110	809	145..1566	2448
	NT2R120058510	810	107..2050	2449
	NT2R120060710	811	274..1278	2450
	NT2R120060720	812	78..2354	2451
15	NT2R120061270	813	14..352	2452
	NT2R120061830	814	906..1580	2453
	NT2R120062100	815	1465..2487	2454
	NT2R120063450	816	278..745	2455
	NT2R120064120	817	281..1321	2456
20	NT2R120064870	818	647..1138	2457
	NT2R120065080	819	63..1193	2458
	NT2R120065530	820	644..1135	2459
	NT2R120066670	821	23..598	2460
25	NT2R120066790	822	272..1747	2461
	NT2R120066820	823	145..1173	2462
	NT2R120067030	824	58..1368	2463
	NT2R120067350	825	100..>2451	2464
	NT2R120067680	826	25..732	2465
30	NT2R120068250	827	123..2246	2466
	NT2R120068550	828	250..1656	2467
	NT2R120070480	829	483..1844	2468
	NT2R120070840	830	25..600	2469
35	NT2R120070960	831	212..>2749	2470
	NT2R120071160	832	921..1643	2471
	NT2R120071330	833	159..2105	2472
	NT2R120071480	834	82..1155	2473
	NT2R120072140	835	845..1192	2474
40	NT2R120072540	836	483..1394	2475
	NT2R120073030	837	914..1351	2476
	NT2R120073840	838	202..1569	2477
	NT2R120073860	839	150..506	2478
45	NT2R120074390	840	60..1916	2479
	NT2R120074690	841	430..>2130	2480
	NT2R120074980	842	175..1269	2481
	NT2R120075070	843	1064..1513	2482
	NT2R120075720	844	193..1758	2483
50	NT2R120075890	845	927..1520	2484
	NT2R120077230	846	79..741	2485
	NT2R120077290	847	101..793	2486
	NT2R120077510	848	455..766	2487
	NT2R120077540	849	527..1075	2488
55	NT2R120078270	850	61..717	2489
	NT2R120078790	851	391..1020	2490
	NT2R120078840	852	635..2410	2491

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	NT2RI20078910	853	334..1524	2492
	NT2RI20080500	854	229..1767	2493
	NT2RI20081880	855	158..1180	2494
	NT2RI20082210	856	449..1120	2495
10	NT2RI20083360	857	60..1898	2496
	NT2RI20083960	858	164..919	2497
	NT2RI20084810	859	863..1384	2498
	NT2RI20085260	860	347..709	2499
15	NT2RI20085980	861	357..>2020	2500
	NT2RI20086560	862	478..798	2501
	NT2RI20087140	863	108..443	2502
	NT2RI20087490	864	498..1862	2503
20	NT2RI20087910	865	508..1011	2504
	NT2RI20088010	866	316..759	2505
	NT2RI20088120	867	10..684	2506
	NT2RI20089420	868	626..1099	2507
25	NT2RI20090650	869	41..1594	2508
	NT2RI20090660	870	65..1852	2509
	NT2RI20090830	871	988..1713	2510
	NT2RI20091440	872	216..1037	2511
30	NT2RI20092150	873	574..>2918	2512
	NT2RI20092890	874	651..2471	2513
	NT2RI20094060	875	17..1030	2514
	NT2RP60000080	876	2249..2614	2515
35	NT2RP60000170	877	128..928	2516
	NT2RP60000320	878	27..2108	2517
	NT2RP60000350	879	553..1734	2518
	NT2RP60000390	880	455..829	2519
40	NT2RP60000590	881	2067..2381	2520
	NT2RP60000720	882	1136..2104	2521
	NT2RP60000860	883	7..660	2522
	NT2RP60001000	884	474..1694	2523
45	NT2RP60001090	885	442..2136	2524
	NT2RP60001230	886	78..1937	2525
	NT2RP60001270	887	858..1652	2526
	NT2RP70000410	888	801..1103	2527
50	NT2RP70000690	889	259..3270	2528
	NT2RP70000760	890	954..1295	2529
	NT2RP70002380	891	231..1208	2530
	NT2RP70002590	892	202..993	2531
55	NT2RP70002710	893	26A..1619	2532
	NT2RP70003640	894	2617..2994	2533
	NT2RP70003910	895	1492..1797	2534
	NT2RP70004250	896	261..1115	2535
55	NT2RP70004770	897	1132..2541	2536
	NT2RP70005790	898	940..1257	2537
	NT2RP70006240	899	26..1756	2538
	NT2RP70008120	900	90..476	2539
	NT2RP70009060	901	2197..3105	2540

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	NT2RP70010800	902	132..2060	2541
	NT2RP70011660	903	5..3619	2542
	NT2RP70012310	904	8..1756	2543
	NT2RP70013060	905	1533..2693	2544
10	NT2RP70013350	906	396..2096	2545
	NT2RP70015910	907	14..1492	2546
	NT2RP70018560	908	167..1561	2547
	NT2RP70021510	909	209..538	2548
15	NT2RP70022430	910	269..2617	2549
	NT2RP70023760	911	92..3292	2550
	NT2RP70023790	912	1022..2797	2551
	NT2RP70024490	913	223..888	2552
20	NT2RP70024500	914	333..1652	2553
	NT2RP70025540	915	191..532	2554
	NT2RP70026190	916	1277..>3059	2555
	NT2RP70028290	917	52..2169	2556
25	NT2RP70028410	918	363..983	2557
	NT2RP70028750	919	69..1226	2558
	NT2RP70029060	920	283..2847	2559
	NT2RP70029820	921	199..2325	2560
30	NT2RP70030500	922	58..480	2561
	NT2RP70030550	923	148..1854	2562
	NT2RP70030910	924	2186..2785	2563
	NT2RP70032030	925	214..1584	2564
35	NT2RP70033040	926	294..1166	2565
	NT2RP70036290	927	490..2808	2566
	NT2RP70036320	928	550..1002	2567
	NT2RP70036470	929	340..3312	2568
40	NT2RP70036800	930	151..2307	2569
	NT2RP70039600	931	254..3121	2570
	NT2RP70040800	932	592..1587	2571
	NT2RP70042040	933	855..1946	2572
45	NT2RP70042330	934	434..2908	2573
	NT2RP70042600	935	428..2539	2574
	NT2RP70043730	936	312..2828	2575
	NT2RP70043960	937	17..3181	2576
50	NT2RP70045410	938	82..>3154	2577
	NT2RP70046560	939	41..2593	2578
	NT2RP70046870	940	47..2995	2579
	NT2RP70047510	941	29..394	2580
55	NT2RP70047660	942	958..1332	2581
	NT2RP70047900	943	1553..1870	2582
	NT2RP70049150	944	436..2349	2583
	NT2RP70049250	945	100..1356	2584
	NT2RP70049750	946	1483..2013	2585
	NT2RP70052050	947	2014..2481	2586
	NT2RP70052190	948	24..413	2587
	NT2RP70054680	949	1192..1563	2588
	NT2RP70054930	950	214..579	2589

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	NT2RP70055020	951	774..1142	2590
	NT2RP70055130	952	175..1791	2591
	NT2RP70055200	953	1388..1879	2592
	NT2RP70061620	954	1241..2518	2593
10	NT2RP70061880	955	161..>3222	2594
	NT2RP70062960	956	604..3786	2595
	NT2RP70063040	957	277..1701	2596
	NT2RP70063740	958	525..908	2597
15	NT2RP70064080	959	189..974	2598
	NT2RP70064900	960	74..2332	2599
	NT2RP70065270	961	261..2756	2600
	NT2RP70066210	962	1294..1926	2601
20	NT2RP70067010	963	342..662	2602
	NT2RP70069800	964	1520..1972	2603
	NT2RP70069860	965	132..1964	2604
	NT2RP70071140	966	1812..2342	2605
25	NT2RP70071540	967	694..1776	2606
	NT2RP70071770	968	28..2103	2607
	NT2RP70072210	969	205..1944	2608
	NT2RP70072520	970	79..>3136	2609
30	NT2RP70073590	971	2133..2525	2610
	NT2RP70073810	972	171..683	2611
	NT2RP70074060	973	248..739	2612
	NT2RP70074220	974	367..726	2613
35	NT2RP70075040	975	365..>3111	2614
	NT2RP70075370	976	253..1710	2615
	NT2RP70078100	977	280..2415	2616
	NT2RP70078170	978	74..1717	2617
40	NT2RP70078430	979	461..2788	2618
	NT2RP70079250	980	365..3256	2619
	NT2RP70079300	981	240..554	2620
	NT2RP70079750	982	954..2867	2621
45	NT2RP70081330	983	187..1458	2622
	NT2RP70081370	984	279..2876	2623
	NT2RP70081420	985	1246..1719	2624
	NT2RP70081440	986	1013..1501	2625
50	NT2RP70081670	987	47..3034	2626
	NT2RP70083150	988	118..>3979	2627
	NT2RP70084060	989	47..847	2628
	NT2RP70084410	990	115..>3256	2629
55	NT2RP70084870	991	70..1422	2630
	NT2RP70085500	992	170..3274	2631
	NT2RP70085570	993	302..2035	2632
	NT2RP70086230	994	799..1203	2633
55	NT2RP70087200	995	211..2583	2634
	NT2RP70088550	996	57..1529	2635
	NT2RP70090120	997	52..2397	2636
	NT2RP70090190	998	1358..2545	2637
	NT2RP70091490	999	18..764	2638

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	NT2RP70091680	1000	2064..2618	2639
	NT2RP70092150	1001	5..481	2640
	NT2RP70092360	1002	116..>3870	2641
	NT2RP70092590	1003	148..2256	2642
10	NT2RP70093220	1004	333..2783	2643
	NT2RP70093630	1005	1372..1710	2644
	NT2RP70093700	1006	124..2220	2645
	NT2RP70093730	1007	212..2389	2646
15	NT2RP70093940	1008	135..2909	2647
	NT2RP70093970	1009	830..1705	2648
	NT2RP70094290	1010	705..1046	2649
	NT2RP70094660	1011	76..393	2650
20	NT2RP70094810	1012	94..3705	2651
	NT2RP70094980	1013	38..2905	2652
	NT2RP70095020	1014	2451..2768	2653
	NT2RP70095070	1015	228..638	2654
25	NTONG10000330	1016	9..2423	2655
	NTONG10000520	1017	83..1501	2656
	NTONG10000980	1018	576..1703	2657
	NTONG10001230	1019	318..1987	2658
30	NTONG10001300	1020	223..1839	2659
	NTONG10001820	1021	677..1558	2660
	NTONG10002140	1022	14..1207	2661
	NTONG10002460	1023	242..1561	2662
35	NTONG10002570	1024	107..658	2663
	NTONG10002640	1025	263..2131	2664
	NTONG20002650	1026	177..2696	2665
	NTONG20003340	1027	322..996	2666
40	NTONG20003630	1028	183..>2114	2667
	NTONG20004920	1029	1693..1998	2668
	NTONG20005830	1030	268..624	2669
	NTONG20008000	1031	160..1503	2670
45	NTONG20008780	1032	264..1829	2671
	NTONG20009660	1033	12..1199	2672
	NTONG20009650	1034	32..388	2673
	NTONG20011370	1035	123..440	2674
50	NTONG20012220	1036	109..447	2675
	NTONG20014280	1037	47..367	2676
	NTONG20015500	1038	388..1416	2677
	NTONG20016120	1039	27..2267	2678
55	OCBBF10000420	1040	457..894	2679
	OCBBF10000870	1041	694..1149	2680
	OCBBF10000860	1042	1..465	2681
	OCBBF10000910	1043	397..3999	2682
55	OCBBF10001040	1044	869..1288	2683
	OCBBF10001180	1045	108..977	2684
	OCBBF10001190	1046	171..2444	2685
	OCBBF10001220	1047	235..2259	2686
	OCBBF20000130	1048	211..2301	2687

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	OCBBF20001260	1049	1733..2107	2688
	OCBBF20002310	1050	302..1870	2689
	OCBBF20002770	1051	19..1374	2690
	OCBBF20002870	1052	1874..>2191	2691
10	OCBBF20007190	1053	457..2277	2692
	OCBBF20008240	1054	46..2169	2693
	OCBBF20009040	1055	273..2030	2694
	OCBBF20009980	1056	152..526	2695
15	OCBBF20010750	1057	221..655	2696
	OCBBF20011010	1058	1..1323	2697
	OCBBF20011240	1059	313..>2823	2698
	OCBBF20011400	1060	144..>3731	2699
20	OCBBF20011760	1061	139..1815	2700
	OCBBF20012100	1062	107..1840	2701
	OCBBF20013070	1063	177..1199	2702
	OCBBF20014020	1064	174..>2999	2703
25	OCBBF20014080	1065	80..646	2704
	OCBBF20014940	1066	160..3648	2705
	OCBBF20015270	1067	539..>2338	2706
	OCBBF20015280	1068	79..>2727	2707
30	OCBBF20015860	1069	201..827	2708
	OCBBF20017060	1070	1065..1463	2709
	PANCR10000210	1071	42..863	2710
	PANCR10001850	1072	77..379	2711
35	PEBLM10000290	1073	1294..1722	2712
	PEBLM10000340	1074	12..1814	2713
	PEBLM10000680	1075	1330..1923	2714
	PEBLM10001440	1076	154..2799	2715
40	PEBLM10001800	1077	1072..1509	2716
	PEBLM20000300	1078	1538..2563	2717
	PEBLM20001120	1079	175..2934	2718
	PEBLM20001260	1080	2535..2918	2719
45	PEBLM20001470	1081	306..698	2720
	PEBLM20002130	1082	35..979	2721
	PEBLM20002480	1083	162..1334	2722
	PEBLM20002700	1084	170..1762	2723
50	PEBLM20003080	1085	669..1685	2724
	PEBLM20003950	1086	285..881	2725
	PEBLM20004790	1087	341..1798	2726
	PLACE50000370	1088	986..1912	2727
55	PLACE50000580	1089	387..3224	2728
	PLACE50000670	1090	2506..2874	2729
	PLACE50000680	1091	407..2119	2730
	PLACE50000800	1092	488..>3266	2731
55	PLACE50001050	1093	417..2234	2732
	PLACE50001130	1094	12..4397	2733
	PLACE50001530	1095	1874..2224	2734
	PLACE50001700	1096	80..2140	2735
	PLACE60000440	1097	1255..1575	2736

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	PLACE60000700	1098	250..684	2737
	PLACE60000800	1099	1570..1995	2738
	PLACE60001370	1100	1126..1521	2739
	PLACE60002050	1101	243..1175	2740
10	PLACE60002630	1102	1574..2191	2741
	PLACE60003710	1103	1170..1517	2742
	PLACE60003790	1104	908..1564	2743
	PLACE60004240	1105	243..845	2744
15	PLACE60004290	1106	1792..2154	2745
	PLACE60005230	1107	449..994	2746
	PLACE60005500	1108	447..791	2747
	PLACE60005550	1109	140..631	2748
20	PLACE60009530	1110	8..337	2749
	PLACE60012810	1111	76..2601	2750
	PLACE60012940	1112	159..587	2751
	PLACE60014430	1113	215..1816	2752
25	PLACE60018880	1114	94..1614	2753
	PLACE60019230	1115	174..524	2754
	PLACE60019250	1116	1562..>2068	2755
	PLACE60020180	1117	41..412	2756
30	PLACE60020840	1118	654..1382	2757
	PLACE60021020	1119	106..600	2758
	PLACE60021510	1120	261..1871	2759
	PLACE60024190	1121	15..1145	2760
35	PLACE60026680	1122	332..1924	2761
	PLACE60026920	1123	1..333	2762
	PLACE60026990	1124	39..836	2763
	PLACE60029490	1125	130..477	2764
40	PLACE60030380	1126	28..1149	2765
	PLACE60030940	1127	61..720	2766
	PLACE60031090	1128	650..1270	2767
	PLACE60032040	1129	110..448	2768
45	PLACE60033720	1130	595..1053	2769
	PLACE60033990	1131	403..1173	2770
	PLACE60037050	1132	485..1159	2771
	PLACE60037400	1133	597..923	2772
50	PLACE60037450	1134	112..558	2773
	PLACE60038500	1135	734..1264	2774
	PLACE60040050	1136	15..599	2775
	PLACE60043120	1137	162..731	2776
55	PLACE60043360	1138	1899..2225	2777
	PLACE60043960	1139	129..1754	2778
	PLACE60043970	1140	208..1842	2779
	PLACE60044540	1141	22...>2582	2780
55	PLACE60044640	1142	319..2100	2781
	PLACE60044910	1143	1249..1572	2782
	PLACE60046630	1144	1108..1620	2783
	PLACE60046870	1145	37..471	2784
	PLACE60047380	1146	384..1250	2785

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	PLACE60049310	1147	18..320	2785
	PLACE60049930	1148	1324..1641	2787
	PLACE60050290	1149	220..606	2788
	PROST10001520	1150	1847..2149	2789
10	PROST10001670	1151	608..1660	2790
	PROST10002200	1152	137..988	2791
	PROST10002460	1153	1240..1713	2792
	PROST10002720	1154	114..689	2793
15	PROST10003430	1155	259..2445	2794
	PROST10005260	1156	1214..1591	2795
	PROST10005360	1157	240..2477	2796
	PROST10005640	1158	139..525	2797
20	PROST20000360	1159	1580..1969	2798
	PROST20000530	1160	1439..1825	2799
	PROST20001760	1161	44..1276	2800
	PROST20002060	1162	1072..1506	2801
25	PROST20002670	1163	547..897	2802
	PROST20002730	1164	1070..1477	2803
	PROST20002740	1165	1557..1910	2804
	PROST20003250	1166	96..965	2805
30	PROST20004630	1167	495..815	2806
	PROST20017390	1168	122..505	2807
	PROST20017960	1169	1401..1829	2808
	PROST20018230	1170	89..1447	2809
35	PROST20018990	1171	2024..2953	2810
	PROST20019980	1172	1544..1852	2811
	PROST20021620	1173	1439..1918	2812
	PROST20023380	1174	11..559	2813
40	PROST20025910	1175	94..408	2814
	PROST20026820	1176	411..1511	2815
	PROST20028420	1177	1173..1607	2816
	PROST20029600	1178	245..856	2817
45	PROST20031020	1179	20..1456	2818
	PROST20031170	1180	163..1578	2819
	PROST20032100	1181	82..1671	2820
	PROST20032320	1182	2537..3004	2821
50	PROST20033020	1183	1550..1906	2822
	PROST20033030	1184	247..567	2823
	PROST20033380	1185	19..1524	2824
	PROST20033400	1186	294..647	2825
55	PROST20034720	1187	280..1764	2826
	PROST20037320	1188	1001..1414	2827
	PROST20039220	1189	1790..2416	2828
	PROST20043320	1190	278..1843	2829
55	PROST20044160	1191	435..866	2830
	PROST20044810	1192	1442..1759	2831
	PROST20051210	1193	405..1217	2832
	PROST20051430	1194	76..540	2833
	PROST20054260	1195	56..952	2834

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	PROST20056040	1196	1235..1552	2635
	PROST20058800	1197	179..493	2636
	PROST20059190	1198	94..483	2637
	PROST20059430	1199	1475..1792	2638
10	PROST20061960	1200	7..393	2639
	PROST20062600	1201	145..2367	2640
	PROST20064500	1202	146..466	2641
	PROST20067370	1203	1219..1944	2642
15	PROST20069880	1204	45..2252	2643
	PROST20072370	1205	139..2256	2644
	PROST20072890	1206	1664..2632	2645
	PROST20073170	1207	166..1905	2646
20	PROST20073890	1208	1022..1324	2647
	PROST20079740	1209	147..527	2648
	PROST20085160	1210	63..734	2649
	PROST20094830	1211	58..2328	2650
25	PUAEN10000570	1212	127..2220	2651
	PUAEN10000810	1213	318..2234	2652
	PUAEN10001610	1214	582..3794	2653
	PUAEN10003220	1215	173..946	2654
30	SALGL10000050	1216	298..933	2655
	SALGL10000470	1217	11..619	2656
	SALGL10000650	1218	193..543	2657
	SALGL10001570	1219	269..1282	2658
35	SKMUS10000140	1220	68..1234	2659
	SKMUS10000220	1221	102..1367	2660
	SKMUS10000640	1222	137..1198	2661
	SKMUS10001040	1223	240..1100	2662
40	SKMUS10001180	1224	300..1076	2663
	SKMUS10001240	1225	35..>1069	2664
	SKMUS10001290	1226	66..749	2665
	SKMUS10001770	1227	203..1276	2666
45	SKMUS20000740	1228	26..1135	2667
	SKMUS20001170	1229	105..1019	2668
	SKMUS20002710	1230	17..1174	2669
	SKMUS20003430	1231	163..861	2670
50	SKMUS20003650	1232	32..388	2671
	SKMUS20003900	1233	135.. 1112	2672
	SKMUS20004580	1234	166..>1905	2673
	SKMUS20004670	1235	141..443	2674
55	SKMUS20004680	1236	4..453	2675
	SKMUS20007240	1237	107..1120	2676
	SKMUS20007740	1238	66..1061	2677
	SKMUS20008470	1239	183..524	2678
55	SKMUS20008630	1240	294..1727	2679
	SKMUS20009020	1241	396..1631	2680
	SKMUS20009330	1242	96..752	2681
	SKMUS20009450	1243	796..1149	2682
	SKMUS20009540	1244	193..1260	2683

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	SKMUS20010080	1245	210..839	2884
	SKMUS20011290	1246	116..1375	2885
	SKMUS20011470	1247	255..968	2886
	SKMUS20013540	1248	117..476	2887
	SKMUS20014920	1249	199..942	2888
10	SKMUS20015010	1250	178..921	2889
	SKMUS20015430	1251	53..847	2890
	SKMUS20016080	1252	145..1026	2891
	SKMUS20016310	1253	385..876	2892
15	SKMUS20016340	1254	274..>1622	2893
	SKMUS20016620	1255	30..806	2894
	SKMUS20016680	1256	196..1290	2895
	SKMUS20016710	1257	30..722	2896
	SKNMC10000070	1258	1265..1594	2897
20	SKNMC10000100	1259	296..694	2898
	SKNMC10000190	1260	1219..1578	2899
	SKNMC10000290	1261	388..789	2900
	SKNMC10001100	1262	405..920	2901
25	SKNMC10001590	1263	720..1991	2902
	SKNMC10001680	1264	1187..1927	2903
	SKNMC10002290	1265	1798..2472	2904
	SKNMC10002510	1266	265..2565	2905
	SKNMC10002640	1267	68..718	2906
30	SKNMC20000650	1268	55..1758	2907
	SKNMC20000970	1269	340..2028	2908
	SKNMC20002240	1270	797..1939	2909
	SKNMC20003050	1271	154..>1168	2910
35	SKNMC20003220	1272	351..1091	2911
	SKNMC20003560	1273	69..650	2912
	SKNMC20005930	1274	363..1262	2913
	SKNMC20006120	1275	1178..1589	2914
	SKNMC20010570	1276	79..2085	2915
40	SKNMC20011130	1277	98..955	2916
	SKNMC20015030	1278	1129..1689	2917
	SKNMC20015550	1279	463..1035	2918
	SKNMC20015960	1280	74..>3352	2919
45	SKNSH10000860	1281	786..1250	2920
	SKNSH10001740	1282	361..1458	2921
	SKNSH10003010	1283	464..1669	2922
	SKNSH10003080	1284	389..871	2923
	SKNSH20001510	1285	462..776	2924
50	SKNSH20001630	1286	1087..1596	2925
	SKNSH20003470	1287	390..863	2926
	SMINT10000160	1288	158..1729	2927
	SMINT10000390	1289	740..1045	2928
	SMINT10000420	1290	76..>2645	2929
55	SMINT10000540	1291	97..636	2930
	SMINT10000570	1292	70..1545	2931
	SMINT10000710	1293	1763..>2065	2932

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	SMINT10001000	1294	27..470	2933
	SMINT10001030	1295	415..2226	2934
	SMINT10001180	1296	1176..1487	2935
	SMINT20000180	1297	1466..1879	2936
	SMINT20000400	1298	243..548	2937
10	SMINT20001450	1299	11..718	2938
	SMINT20002270	1300	1427..1819	2939
	SMINT20002390	1301	517..885	2940
	SMINT20002770	1302	220..1167	2941
15	SMINT20003960	1303	5..2851	2942
	SMINT20004000	1304	408..899	2943
	SMINT20005450	1305	1001..1387	2944
	SMINT20005580	1306	1700..2029	2945
	SPLEN10000490	1307	27..1364	2946
20	SPLEN10000910	1308	742..1347	2947
	SPLEN10001430	1309	165..695	2948
	SPLEN20000200	1310	1974..2282	2949
	SPLEN20000470	1311	1030..1560	2950
25	SPLEN20000720	1312	808..1842	2951
	SPLEN20001340	1313	61..1146	2952
	SPLEN20001970	1314	414..1310	2953
	SPLEN20002420	1315	661..1191	2954
	SPLEN20002430	1316	344..763	2955
30	SPLEN20002670	1317	1638..>3316	2956
	SPLEN20002700	1318	69..440	2957
	SPLEN20003100	1319	1001..1321	2958
	SPLEN20003570	1320	928..2322	2959
35	SPLEN20004430	1321	509..817	2960
	SPLEN20004960	1322	1792..2175	2961
	SPLEN20005410	1323	12..824	2962
	STOMA10000470	1324	135..533	2963
	STOMA10000520	1325	1790..2170	2964
40	STOMA10001170	1326	196..1818	2965
	STOMA10001330	1327	410..1858	2966
	STOMA10001860	1328	364..1476	2967
	STOMA20000320	1329	943..1278	2968
45	STOMA20000880	1330	1825..2286	2969
	STOMA20001210	1331	196..1458	2970
	STOMA20001880	1332	1068..1757	2971
	STOMA20002570	1333	429..746	2972
	STOMA20002890	1334	187..801	2973
50	STOMA20003960	1335	591..1748	2974
	STOMA20004780	1336	129..554	2975
	STOMA20004820	1337	206..1228	2976
	SYNOV10001280	1338	111..2084	2977
	SYNOV10001640	1339	206..1033	2978
55	SYNOV20001770	1340	359..673	2979
	SYNOV20002910	1341	1085..1750	2980
	SYNOV20008200	1342	461..>2203	2981

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	SYNOV20010140	1343	72..458	2982
	SYNOV20011440	1344	275..1468	2983
	SYNOV20013740	1345	147..1472	2984
	SYNOV20014510	1346	89..982	2985
10	SYNOV20014570	1347	1488..1811	2986
	SYNOV20016480	1348	132..656	2987
	TEST110000230	1349	1101..1415	2988
	TEST110000250	1350	167..2032	2989
15	TEST110000420	1351	175..1863	2990
	TEST110000510	1352	75..2297	2991
	TEST110000550	1353	46..1185	2992
	TEST110000640	1354	106..1950	2993
20	TEST110000700	1355	225..2042	2994
	TEST110000960	1356	274..978	2995
	TEST110001250	1357	1027..1641	2996
	TEST110001270	1358	208..1581	2997
25	TEST110001310	1359	38..1549	2998
	TEST110001380	1360	732..1868	2999
	TEST110001630	1361	249..1298	3000
	TEST110001680	1362	134..1390	3001
30	TEST110001790	1363	1577..1936	3002
	TEST110001910	1364	935..1786	3003
	TEST120000180	1365	234..563	3004
	TEST120000440	1366	166..2238	3005
35	TEST120001200	1367	664..1059	3006
	TEST120001540	1368	230..1684	3007
	TEST120001770	1369	1209..2447	3008
	TEST120001790	1370	154..747	3009
40	TEST120001840	1371	16..1962	3010
	TEST120002070	1372	1161..1631	3011
	TEST120002080	1373	1784..2425	3012
	TEST120002380	1374	528..1859	3013
45	TEST120002530	1375	289..1071	3014
	TEST120003560	1376	654..1013	3015
	TEST120003720	1377	578..1144	3016
	TEST120004350	1378	97..726	3017
50	TEST120004820	1379	916..1833	3018
	TEST120005200	1380	192..1379	3019
	TEST120005910	1381	30..1469	3020
	TEST120006000	1382	645..1682	3021
55	TEST120006270	1383	72..>2174	3022
	TEST120006710	1384	334..645	3023
	TEST120006950	1385	68..>2012	3024
	TEST120006990	1386	134..2155	3025
60	TEST120007070	1387	56..1084	3026
	TEST120007620	1388	125..961	3027
	TEST120007840	1389	36..3281	3028
	TEST120008190	1390	820..1236	3029
	TEST120008300	1391	323..1186	3030

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	TESTI20008490	1392	59..1333	3031
	TESTI20008830	1393	1131..1718	3032
	TESTI20009090	1394	562..894	3033
	TESTI20009510	1395	225..1115	3034
	TESTI20009700	1396	84..1628	3035
10	TESTI20010080	1397	1565..>2060	3036
	TESTI20010490	1398	730..2349	3037
	TESTI20010820	1399	1609..1926	3038
	TESTI20011340	1400	243..1346	3039
15	TESTI20011410	1401	425..2725	3040
	TESTI20011800	1402	228..1178	3041
	TESTI20012370	1403	257..2071	3042
	TESTI20012690	1404	660..2603	3043
	TESTI20013060	1405	125..427	3044
20	TESTI20013300	1406	22..>2563	3045
	TESTI20013450	1407	187..1917	3046
	TESTI20013520	1408	334..759	3047
	TESTI20014120	1409	185..1384	3048
25	TESTI20014200	1410	214..1299	3049
	TESTI20015110	1411	61..2058	3050
	TESTI20015120	1412	565..1287	3051
	TESTI20015560	1413	400..1326	3052
	TESTI20015930	1414	1157..1468	3053
30	TESTI20016210	1415	1121..1474	3054
	TESTI20016610	1416	280..3345	3055
	TESTI20016650	1417	2190..2549	3056
	TESTI20016710	1418	1071..2003	3057
35	TESTI20017580	1419	143..676	3058
	TESTI20017660	1420	317..652	3059
	TESTI20017920	1421	84..890	3060
	TESTI20018150	1422	815..1993	3061
	TESTI20018260	1423	310..1113	3062
40	TESTI20018270	1424	19..1899	3063
	TESTI20018290	1425	337..>2156	3064
	TESTI20018520	1426	46..2211	3065
	TESTI20018620	1427	1355..1729	3066
45	TESTI20018690	1428	1178..2425	3067
	TESTI20018790	1429	481..1821	3068
	TESTI20018980	1430	146..559	3069
	TESTI20019500	1431	126..1403	3070
	TESTI20019680	1432	1168..1509	3071
50	TESTI20019910	1433	345..1601	3072
	TESTI20020020	1434	1547..>1884	3073
	TESTI20020480	1435	255..569	3074
	TESTI20020570	1436	217..1317	3075
55	TESTI20020810	1437	194..1498	3076
	TESTI20020900	1438	81..1547	3077
	TESTI20021050	1439	68..2689	3078
	TESTI20021490	1440	45..1814	3079

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	TESTI20022230	1441	205..783	3080
	TESTI20022450	1442	59..1333	3081
	TESTI20022510	1443	97..2217	3082
	TESTI20022560	1444	17..2494	3083
10	TESTI20022640	1445	260..913	3084
	TESTI20022940	1446	41..469	3085
	TESTI20023610	1447	365..949	3086
	TESTI20023690	1448	336..1160	3087
15	TESTI20024150	1449	400..1080	3088
	TESTI20024230	1450	125..1339	3089
	TESTI20024610	1451	181..1605	3090
	TESTI20024650	1452	45..1829	3091
20	TESTI20024670	1453	1375..1845	3092
	TESTI20024980	1454	261..1889	3093
	TESTI20025160	1455	133..1164	3094
	TESTI20025440	1456	293..1819	3095
25	TESTI20025800	1457	60..1022	3096
	TESTI20026320	1458	31..414	3097
	TESTI20026760	1459	830..1663	3098
	TESTI20026980	1460	212..1354	3099
30	TESTI20027000	1461	22..573	3100
	TESTI20027070	1462	88..1410	3101
	TESTI20027290	1463	158..1333	3102
	TESTI20027890	1464	104..>1506	3103
35	TESTI20028060	1465	1596..1970	3104
	TESTI20028400	1466	740..1066	3105
	TESTI20028660	1467	1111..1995	3106
	TESTI20029120	1468	295..1920	3107
40	TESTI20029550	1469	391..1446	3108
	TESTI20030050	1470	21..800	3109
	TESTI20030370	1471	271..1368	3110
	TESTI20030590	1472	1028..1474	3111
45	TESTI20030710	1473	88..666	3112
	TESTI20030740	1474	85..2055	3113
	TESTI20031090	1475	28..>2034	3114
	TESTI20031170	1476	188..1660	3115
50	TESTI20031300	1477	157..2004	3116
	TESTI20031520	1478	150..1862	3117
	TESTI20031930	1479	474..1010	3118
	TESTI20031960	1480	32..>1839	3119
55	TESTI20032280	1481	189..560	3120
	TESTI20032550	1482	242..670	3121
	TESTI20032800	1483	1445..1873	3122
	TESTI20032990	1484	49..411	3123
60	TESTI20033250	1485	98..2041	3124
	TESTI20033270	1486	48..722	3125
	TESTI20033540	1487	311..1930	3126
	TESTI20033560	1488	193..1296	3127
	TESTI20033760	1489	294..659	3128

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	TESTI20034130	1490	109..>2444	3129
	TESTI20034180	1491	1113..1484	3130
	TESTI20034190	1492	120..1520	3131
	TESTI20034980	1493	265..1185	3132
	TESTI20035120	1494	321..2585	3133
10	TESTI20035410	1495	735..1208	3134
	TESTI20035510	1496	734..1741	3135
	TESTI20035740	1497	41..1651	3136
	TESTI20035800	1498	1263..1583	3137
15	TESTI20035890	1499	206..1507	3138
	TESTI20036250	1500	45..2216	3139
	TESTI20036490	1501	88..459	3140
	TESTI20037270	1502	33..1391	3141
	TESTI20037810	1503	128..520	3142
20	TESTI20038940	1504	1166..1630	3143
	TESTI20039140	1505	73..1530	3144
	TESTI20039980	1506	2..514	3145
	TESTI20040000	1507	291..881	3146
25	TESTI20040310	1508	126..1463	3147
	TESTI20041110	1509	143..502	3148
	TESTI20041220	1510	33..1703	3149
	TESTI20042070	1511	95..1903	3150
	TESTI20042290	1512	647..1711	3151
30	TESTI20042430	1513	1227..1535	3152
	TESTI20042870	1514	1697..2263	3153
	TESTI20042950	1515	187..1887	3154
	TESTI20047120	1516	112..1002	3155
35	TESTI20049290	1517	402..1226	3156
	TESTI20049820	1518	157..1875	3157
	TESTI20049940	1519	50..550	3158
	TESTI20051550	1520	79..501	3159
	TESTI20052680	1521	60..1247	3160
40	TESTI20053960	1522	402..2522	3161
	TESTI20054080	1523	108..929	3162
	TESTI20054920	1524	137..568	3163
	TESTI20055840	1525	210..1214	3164
45	TESTI20056900	1526	124..1788	3165
	TESTI20057310	1527	287..>1853	3166
	TESTI20057420	1528	164..1636	3167
	TESTI20058600	1529	430..1167	3168
	TESTI20062380	1530	719..1567	3169
50	TESTI20062550	1531	511..837	3170
	TESTI20064250	1532	537..1436	3171
	TESTI20064830	1533	373..1614	3172
	TESTI20065720	1534	222..644	3173
55	TESTI20067740	1535	382..1239	3174
	TESTI20068660	1536	87..1337	3175
	TESTI20068720	1537	378..1331	3176
	TESTI20069780	1538	310..639	3177

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	TESTI20069790	1539	887..1189	3178
	TESTI20071830	1540	352..1176	3179
	TESTI20073580	1541	3..1394	3180
	TESTI20074020	1542	1097..1426	3181
10	TESTI20074640	1543	204..>1824	3182
	TESTI20074660	1544	124..1683	3183
	TESTI20074800	1545	81..2000	3184
	TESTI20076130	1546	122..>2107	3185
15	TESTI20077490	1547	852..1598	3186
	TESTI20077500	1548	391..1722	3187
	TESTI20078140	1549	897..1400	3188
	TESTI20078640	1550	287..802	3189
20	TESTI20078670	1551	318..1952	3190
	TESTI20078720	1552	92..1309	3191
	TESTI20079510	1553	824..3025	3192
	TESTI20080200	1554	153..2429	3193
25	TESTI20080330	1555	72..497	3194
	TESTI20081390	1556	118..1839	3195
	TESTI20081440	1557	147..545	3196
	TESTI20082340	1558	931..1419	3197
30	TESTI20082400	1559	409..834	3198
	TESTI20083430	1560	157..2979	3199
	TESTI20083870	1561	31..552	3200
	TESTI20084400	1562	1749..2078	3201
35	TESTI20086570	1563	246..1289	3202
	TESTI20087740	1564	14..1900	3203
	TESTI20088470	1565	362..757	3204
	TESTI20136910	1566	1667..2026	3205
40	TESTI20138320	1567	98..1060	3206
	TESTI20140360	1568	831..1349	3207
	TESTI20177400	1569	70..1584	3208
	TESTI30000020	1570	97..1914	3209
45	THYMU10000020	1571	286..1131	3210
	THYMU10000320	1572	1299..1691	3211
	THYMU10000830	1573	1169..1936	3212
	THYMU10001050	1574	632..934	3213
50	THYMU10001760	1575	1..492	3214
	THYMU10002910	1576	1598..2026	3215
	THYMU10003290	1577	22..534	3216
	THYMU10003590	1578	743..2005	3217
55	THYMU10003660	1579	1749..2084	3218
	THYMU10003820	1580	1242..1601	3219
	THYMU10004590	1581	594..1142	3220
	THYMU10004730	1582	421..735	3221
60	THYMU10004910	1583	301..1119	3222
	THYMU10005270	1584	1706..>2057	3223
	THYMU10005580	1585	896..1819	3224
	THYMU20001400	1586	42..410	3225
	THYMU20002360	1587	2..385	3226

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Table 1 (continued)

	Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5	THYMU20003170	1588	703..1041	3227
	THYMU20003690	1589	328..1782	3228
	TRACH10000180	1590	63..1205	3229
	TRACH10000300	1591	384..902	3230
10	TRACH10000570	1592	722..1039	3231
	TRACH10000630	1593	431..1372	3232
	TRACH10000740	1594	80..1672	3233
	TRACH10001000	1595	181..660	3234
15	TRACH10001060	1596	744..1121	3235
	TRACH10001250	1597	21..1610	3236
	TRACH10001400	1598	266..622	3237
	TRACH20000150	1599	1303..1755	3238
20	TRACH20000790	1600	47..385	3239
	TRACH20001850	1601	19..750	3240
	TRACH20001960	1602	144..974	3241
	TRACH20002350	1603	1123..1437	3242
25	TRACH20002370	1604	197..1471	3243
	TRACH20002500	1605	120..1682	3244
	TRACH20002890	1606	895..2022	3245
	TRACH20003930	1607	1403..>2562	3246
30	TRACH20004110	1608	150..1844	3247
	TRACH20004200	1609	80..>2895	3248
	TRACH20004610	1610	498..2084	3249
	TRACH20004720	1611	435..1940	3250
35	TRACH20004960	1612	115..1842	3251
	TRACH20004970	1613	1083..1517	3252
	TRACH20006850	1614	208..1866	3253
	TRACH20006750	1615	232..1200	3254
40	TRACH20007870	1616	1147..1452	3255
	TRACH20007800	1617	492..1937	3256
	TRACH20008940	1618	701..1957	3257
	TRACH20008980	1619	350..661	3258
45	TRACH20009260	1620	75..770	3259
	TRACH20009440	1621	879..1235	3260
	TRACH20011920	1622	530..>2034	3261
	TRACH20012890	1623	143..715	3262
50	TRACH20013950	1624	1697..2602	3263
	TRACH20014000	1625	1626..1949	3264
	TRACH20015920	1626	569..877	3265
	TRACH20016070	1627	484..1176	3266
55	UMVEN10001220	1628	698..1339	3267
	UMVEN20001330	1629	164..2242	3268
	UTERU10000770	1630	2074..2418	3269
	UTERU10000960	1631	952..1593	3270
55	UTERU10001600	1632	527..1747	3271
	UTERU10001920	1633	112..474	3272
	UTERU20000470	1634	1691..>2197	3273
	UTERU20003380	1635	130..816	3274
	UTERU20003930	1636	514..1101	3275

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Table 1 (continued)

Clone name	SEQ ID NO. of nucleotide sequence	Position of CDS	SEQ ID NO. of amino acid sequence
5 UTERU20004850	1637	385..732	3276
UTERU20005410	1638	432..800	3277
UTERU20005690	1639	217..1899	3278

[0028] Namely, primers used to synthesize polynucleotides can be designed based on the nucleotide sequences of polynucleotides of the present invention shown in SEQ ID NOs in the above Table 1. When one intends to synthesize full-length cDNAs, an oligo dT primer can be used as the 3'-end primer. The length of the primers is usually 15-100 bp, and favorably between 15-35 bp. In case of LA PCR, which is described below, the primer length of 25-35 bp may provide a good result.

[0029] A method to design a primer that enables a specific amplification based on the aimed nucleotide sequence is known to those skilled in the art (Current Protocols in Molecular Biology, Ausubel et al. edit, (1987) John Wiley & Sons, Section 6.1-6.4). In designing a primer based on the 5'-end sequence, the primer is designed so as that, in principle, the amplification products will include the translation start site. Accordingly, for example, when the 5'-end primer is designed based on the nucleotide sequence of 5' untranslated region (5'UTR), any part of the 5'-end, which ensures the specificity to the cDNA of interest, can be selected as the primer.

[0030] When synthesizing a full-length cDNA, the target nucleotide sequence to be amplified can extend to several thousand bp in some cDNA. However, it is possible to amplify such a long nucleotides by using such as LA PCR (Long and Accurate PCR). It is advantageous to use LA PCR when synthesizing long DNA. In LA PCR, in which a special DNA polymerase having 3' → 5' exonuclease activity is used, misincorporated nucleotides can be removed. Accordingly, accurate synthesis of the complementary strand can be achieved even with a long nucleotide sequence. By using LA PCR, it is reported that amplification of a nucleotide with 20 kb longer can be achieved under desirable conditions (Takeshi Hayashi (1996) Jikken-Igaku Bessatsu, "Advanced Technologies in PCR" Youdo-sha).

[0031] A template DNA for synthesizing the full-length cDNA of the present invention can be obtained by using cDNA libraries that are prepared by various methods. The full-length cDNA clones of the present invention are clones with high probability of completeness in length, which were obtained by the method comprising the steps of [1] preparing libraries containing cDNAs with the very high fullness ratio by oligo-capping, and [2] assembling the 5'-end sequences and selecting one with the highest probability of completeness in length in the cluster formed (there are many clones longer in the 5'-end direction).

[0032] However, the uses of primers designed based on the full-length nucleotide sequences provided by the present invention enable easily obtaining full-length cDNAs without such a special technique.

[0033] The problem with the cDNA libraries prepared by the known methods or commercially available is that mRNA contained in the libraries has very low fullness ratio. Thus, it is difficult to screen full-length cDNA clone directly from the library using ordinary cloning methods. The present invention has revealed a nucleotide sequence of novel full-length cDNA. If a full-length nucleotide sequence is provided, it is possible to synthesize a target full-length cDNA by using enzymatic reactions such as PCR. In particular, a full-length-enriched cDNA library, synthesized by methods such as oligo-capping, is desirable to synthesize a full-length cDNA with more reliability.

[0034] The 5'-end sequence of the full-length cDNA clones of the invention can be used to isolate the regulatory element of transcription including the promoter on the genome. A rough draft of the human genome (analysis of human genomic sequence with lower accuracy), which covers 90% of the genome, has been reported (Nature, Vol.409, 814-823, 2001), and by the year 2003, analysis of the entire human genomic sequence is going to be finished. However, it is hard to analyze with software the transcription start sites on the human genome, in which long introns exist. By contrast, it is easy to specify the transcription start site on the genomic sequence using the nucleotide sequence which includes the 5'-end of the full-length cDNA clone of the present invention, and thus it is easy to obtain the genomic region involved in transcription regulation, which includes the promoter that is contained in the upstream of the transcription start site.

[0035] The polypeptide encoded by the full-length cDNA of the invention can be prepared as a recombinant polypeptide or as a natural polypeptide. For example, the recombinant polypeptide can be prepared by inserting the polynucleotide encoding the polypeptide of the invention into a vector, introducing the vector into an appropriate host cell and purifying the polypeptide expressed within the transformed host cell, as described below. In contrast, the natural polypeptide can be prepared, for example, by utilizing an affinity column to which an antibody against the polypeptide of the invention (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 16.1-16.19) is attached. The antibody used for affinity purification may be either a polyclonal antibody, or a monoclonal antibody. Alternatively, *in vitro* translation (See, for example, "On the fidelity of mRNA translation in the nuclease-treated

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rabbit reticulocyte lysate system." Dasso M.C., and Jackson R.J. (1989) *Nucleic Acids Res.* 17: 3129-3144) may be used for preparing the polypeptide of the invention.

[0036] Polypeptides functionally equivalent to the polypeptides of the present invention can be prepared based on the activities, which were clarified in the above-mentioned manner, of the polypeptides of the present invention. Using the biological activity possessed by the polypeptide of the invention as an index, it is possible to verify whether or not a particular polypeptide is functionally equivalent to the polypeptide of the invention by examining whether or not the polypeptide has said activity.

[0037] Polypeptides functionally equivalent to the polypeptides of the present invention can be prepared by those skilled in the art, for example, by using a method for introducing mutations into an amino acid sequence of a polypeptide (for example, site-directed mutagenesis (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 8.1-8.5). Besides, such polypeptides can be generated by polypeptide mutagenesis. The present invention also includes a polypeptide comprising the amino acid sequence shown in Table 1 in which one or more amino acids are substituted, deleted, inserted, and/or added, as long as the polypeptides have the equivalent functions to those of the polypeptides identified in the present Examples described later.

[0038] There are no limitations on the number and sites of amino acid mutations, as long as the polypeptides maintain the functions thereof. The number of mutations typically corresponds to 30% or less, or 20% or less, or 10% or less, preferably 5% or less, or 3% or less of the total amino acids, more preferably 2% or less or 1% or less of the total amino acids. Alternatively, herein, substitution of one or more amino acids includes substitution of several amino acids. As used herein, the term "several amino acids" means, for example, 5 amino acids, preferably 4 or 3 amino acids, more preferably 2 amino acids, and further preferably 1 amino acid.

[0039] From the viewpoint of maintaining the polypeptide function, it is preferable that a substituted amino acid has a similar property to that of the original amino acid. For example, Ala, Val, Leu, Ile, Pro, Met, Phe and Trp are assumed to have similar properties to one another because they are all classified into a group of non-polar amino acids. Similarly, substitution can be performed among non-charged amino acid such as Gly, Ser, Thr, Cys, Tyr, Asn, and Gln, acidic amino acids such as Asp and Glu, and basic amino acids such as Lys, Arg, and His.

[0040] In addition, polypeptides functionally equivalent to the polypeptides of the present invention can be isolated by using techniques of hybridization or gene amplification known to those skilled in the art. Specifically, using the hybridization technique (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 6.3-6.4)), those skilled in the art can usually isolate a polynucleotide highly homologous to the polynucleotide encoding the polypeptide identified in the present Example based on the identified nucleotide sequence (Table 1) or a portion thereof and obtain the functionally equivalent polypeptide from the isolated polynucleotide. The present invention includes polypeptides encoded by the polynucleotides hybridizing with the polynucleotides encoding the polypeptides identified in the present Example, as long as the polypeptides are functionally equivalent to the polypeptides identified in the present Example. Organisms from which the functionally equivalent polypeptides are isolated are illustrated by vertebrates such as human, mouse, rat, rabbit, pig and bovine, but are not limited to these animals.

[0041] Washing conditions of hybridization for the isolation of polynucleotides encoding the functionally equivalent polypeptides are usually "1x SSC, 0.1% SDS, 37°C"; more stringent conditions are "0.5x SSC, 0.1% SDS, 42°C"; and still more stringent conditions are "0.1x SSC, 0.1% SDS, 65°C". Alternatively, the following conditions can be given as hybridization conditions of the present invention. Namely, conditions in which the hybridization is done at "6x SSC, 40% Formamide, 25°C", and the washing at "1x SSC, 55°C" can be given. More preferable conditions are those in which the hybridization is done at "6x SSC, 40% Formamide, 37°C", and the washing at "0.2x SSC, 55°C". Even more preferable are those in which the hybridization is done at "6x SSC, 50% Formamide, 37°C", and the washing at "0.1x SSC, 62°C". The more stringent the conditions of hybridization are, the more frequently the polynucleotides highly homologous to the probe sequence are isolated. Therefore, it is preferable to conduct hybridization under stringent conditions. Examples of stringent conditions in the present invention are, washing conditions of "0.5x SSC, 0.1% SDS, 42°C", or alternatively, hybridization conditions of "6x SSC, 40% Formamide, 37°C", and the washing at "0.2x SSC, 55°C".

[0042] One skilled in the art can suitably select various conditions, such as dilution ratios of SSC, formamide concentrations, and temperatures to accomplish a similar stringency.

[0043] However, the above-mentioned combinations of SSC, SDS and temperature conditions are indicated just as examples. Those skilled in the art can select the hybridization conditions with similar stringency to those mentioned above by properly combining the above-mentioned or other factors (for example, probe concentration, probe length and duration of hybridization reaction) that determines the stringency of hybridization.

[0044] The amino acid sequences of polypeptides isolated by using the hybridization techniques usually have high identity to those of the polypeptides of the present invention, which are shown in Table 1. The present invention encompasses a polynucleotide comprising a nucleotide sequence that has a high identity to the nucleotide sequence of claim 1 (a). Furthermore, the present invention encompasses a peptide, or polypeptide comprising an amino acid sequence that has a high identity to the amino acid sequence encoded by the polynucleotide of claim 1 (b). The term

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"high identity" indicates sequence identity of at least 40% or more; preferably 80% or more; and more preferably 70% or more. Alternatively, more preferable is identity of 90% or more, or 93% or more, or 95% or more, furthermore, 97% or more, or 99% or more. The identity can be determined by using the BLAST search algorithm.

[0045] As used herein, "percent identity" of amino acid sequences or nucleic acids is determined using the algorithm BLAST of Karlin and Altschul (Proc. Natl. Acad. Sci. USA 90:5873-5877, 1993). Such an algorithm is incorporated into the BLASTN and BLASTX programs of Altschul et al. (J. Mol. Biol. 215:403-410, 1990). BLAST nucleotide searches are performed with the BLASTN program, for example, score = 100, wordlength = 12. BLAST protein searches are performed with the BLASTX program, for example, score = 50, wordlength = 3. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs are used. See <http://www.ncbi.nlm.nih.gov>.

[0046] With the gene amplification technique (PCR) (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 6.1-6.4)) using primers designed based on the nucleotide sequence (Table 1) or a portion thereof identified in the present Example, it is possible to isolate a polynucleotide fragment highly homologous to the polynucleotide sequence or a portion thereof and to obtain functionally equivalent polypeptide to a particular polypeptide identified in the present Example based on the isolated polynucleotide fragment.

[0047] The present invention also provides a polynucleotide containing at least 15 nucleotides complementary to a polynucleotide comprising a nucleotide sequence of SEQ ID NOs shown in Table 1 or the complementary strand thereof. Herein, the term "complementary strand" is defined as one strand of a double strand DNA composed of A:T and G:C base pair to the other strand. Also, "complementary" is defined as not only those completely matching within a continuous region of at least 15 nucleotides, but also having a identity of at least 70%, favorably 80% or higher, more favorably 90% or higher, and most favorably 95% or higher within that region. The identity may be determined using the algorithm described herein.

[0048] Such a polynucleotide includes probes and primers used for the detection and amplification of a polynucleotide encoding the inventive polypeptide. When used as a primer, the polynucleotide usually comprises 15 to 100 bp, and preferably of 15 to 35 bp. When used as a probe, the polynucleotide comprises the whole or a part of the sequence of a polynucleotide of the invention, and comprises at least 15 bp. When used as primers, such polynucleotides are complementary at the 3'-end, and restriction enzyme recognition sequences or tags can be added to the 5'-end.

[0049] Furthermore, polynucleotides of the present invention include an antisense polynucleotide for suppressing the expression of a polypeptide of the invention, which comprises an amino acid sequence of SEQ ID NOs shown in Table 1. To exert an antisense effect, an antisense polynucleotide has at least 15 bp or more, for example 50 bp or more, preferably 100 bp or more, and more preferably 500 bp or more, and usually has 3000 bp or less, and preferably 2000 bp or less. Antisense polynucleotides can be used in the gene therapy of diseases caused by abnormalities of the polypeptides of the invention (abnormal function or abnormal expression). An antisense polynucleotide can be prepared, for example, by the phosphorothioate method ("Physicochemical properties of phosphorothioate oligodeoxynucleotides." Stein (1988) Nucleic Acids Res. 16: 3209-3221) based on the sequence information of polynucleotide encoding a polypeptide of the invention (for example, the nucleotide sequences of SEQ ID NO: 1 to 1639).

[0050] The polynucleotides or antisense polynucleotides of the present invention can be used in, for example, gene therapy. As target diseases, for example, cancers or various inflammatory diseases may be preferable. These molecules can be used for gene therapy, for example, by administering them to patients by the *in vivo* or *ex vivo* method using virus vectors such as retrovirus vectors, adenovirus vectors, and adeno-related virus vectors, or non-virus vectors such as liposomes.

[0051] The present invention also includes a partial peptide of the polypeptides of the invention. The partial peptide comprises a polypeptide generated as a result that a signal peptide has been removed from a secretory protein. If the polypeptide of the present invention has an activity as a receptor or a ligand, the partial peptide may function as a competitive inhibitor of the polypeptide and may bind to the receptor (or ligand). In addition, the present invention includes an antigen peptide for raising antibodies. For the peptides to be specific for the polypeptide of the invention, the peptides comprise at least 7 amino acids, preferably 8 amino acids or more, more preferably 9 amino acids or more, and even more preferably 10 amino acids or more. The peptide can be used for preparing antibodies against the polypeptide of the invention, or competitive inhibitors of them, and also screening for a receptor that binds to the polypeptide of the invention. The partial peptides of the invention can be produced, for example, by genetic engineering methods, known methods for synthesizing peptides, or digesting the polypeptide of the invention with an appropriate peptidase.

[0052] The present invention also relates to a vector into which a polynucleotide of the invention is inserted. The vector of the invention is not limited as long as it contains the inserted polynucleotide stably. For example, if *E. coli* is used as a host, vectors such as pBluescript vector (Stratagene) are preferable as a cloning vector. To produce the polypeptide of the invention, expression vectors are especially useful. Any expression vector can be used as long as it is capable of expressing the polypeptide *in vitro*, in *E. coli*, in cultured cells, or *in vivo*. For example, pBEST vector (Promega) is preferable for *in vitro* expression, pET vector (Invitrogen) for *E. coli*, pME18S-FL3 vector (GenBank Accession No. AB009864) for cultured cells, and pME18S vector (Mol. Cell. Biol. (1988) 8: 466-472) for *in vivo* expression.

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To insert the polynucleotide of the invention, ligation utilizing restriction sites can be performed according to the standard method (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 11.4-11.11).

[0053] Recently, the technique of GATEWAY™ system (Invitrogen), which is an expression vector construction system for polypeptide expression, has been developed (Experimental Medicine, Vol. 18, No. 19 (December), p2716-2717, 2000). This system includes two types of site-specific recombinases (BP CLONASE™ and LR CLONASE™) derived from lambda phage and uses BP CLONASE™-specific recombination sites for an Entry Vector and LR CLONASE™-specific recombination sites for a Destination Vector, which may comprise a tag useful for polypeptide purification. With this system, an expression vector can be obtained by using homologous recombination.

[0054] First, a polynucleotide fragment of interest is inserted into the entry vector using the first recombination. Then, the secondary recombination is allowed to take place between the entry vector, where the polynucleotide fragment of interest has been inserted, and the destination vector. Thus, the expression vector can be prepared rapidly and highly efficiently. With the above-mentioned typical method using restriction enzyme and ligase reactions, the step of expression vector construction and expression of polypeptide of interest takes about 7 to 10 days. However, with the GATEWAY™ system, the polypeptide of interest can be expressed and prepared in only 3 to 4 days. Thus, the system ensures a high-throughput functional analysis for expressed polypeptides (<http://biotech.nikkei.co.jp/netlink/ito/gate-way/>).

[0055] The present invention also relates to a transformant carrying the vector of the invention. Any cell can be used as a host into which the vector of the invention is inserted, and various kinds of host cells can be used depending on the purposes. For strong expression of the polypeptide in eukaryotic cells, COS cells or CHO cells can be used, for example.

[0056] Introduction of the vector into host cells can be performed, for example, by calcium phosphate precipitation method, electroporation method (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 9.1-9.9), lipofectamine method (GIBCO-BRL), or microinjection method, etc.

[0057] Further, a polynucleotide containing at least 15 nucleotides comprising a nucleotide sequence of any one of the polynucleotides comprising the nucleotide sequences of SEQ ID NOs shown in Table 1 or the complementary strand thereof can be used not only as a primer for synthesizing full-length cDNAs but also for testing and diagnosing the abnormalities of the polypeptide encoded by the full-length cDNA of the present invention. For example, by utilizing polymerase chain reaction (genomic DNA-PCR, or RT-PCR) using the polynucleotide of the invention as a primer, polynucleotide encoding the polypeptide of the invention can be amplified. It is also possible to obtain the regulatory region of expression in the 5'-upstream by using PCR or hybridization since the transcription start site within the genomic sequence can be easily specified based on the 5'-end sequence of the full-length cDNA. The obtained genomic region can be used for detection and/or diagnosis of the abnormality of the sequence by RFLP analysis, SSCP, or sequencing. Especially, in the case where expression of the mRNA of the present invention varies according to a specific disease, analysis of the amount of expression of the mRNA using the polynucleotide of the present invention as a probe or a primer enables detection and diagnosis of the disease.

[0058] The present invention also relates to antibodies that bind to the polypeptide of the invention. There are no limitations in the form of the antibodies of the invention. They include polyclonal antibodies, monoclonal antibodies, or their portions that can bind to an antigen. They also include antibodies of all classes. Furthermore, special antibodies such as humanized antibodies and chimeric antibodies are also included.

[0059] The polyclonal antibody of the invention can be obtained according to the standard method by synthesizing an oligopeptide corresponding to the amino acid sequence and immunizing rabbits with the peptide (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 11.12-11.13). The monoclonal antibody of the invention can be obtained according to the standard method by purifying the polypeptide expressed in *E. coli*, immunizing mice with the polypeptide, and producing a hybridoma cell by fusing the spleen cells and myeloma cells (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 11.4-11.11).

[0060] The antibody binding to the polypeptide of the present invention can be used for purification of the polypeptide of the invention, and also for detection and/or diagnosis of the abnormalities of the expression and structure of the polypeptide. Specifically, polypeptides can be extracted, for example, from tissues, blood, or cells, and the polypeptide of the invention is detected by Western blotting, immunoprecipitation, or ELISA, etc. for the above purpose.

[0061] Furthermore, the antibody binding to the polypeptide of the present invention can be utilized for treating the diseases that associates with the polypeptide of the invention. If the antibodies are used for treating patients, human antibodies, humanized antibodies, or chimeric antibodies are preferable in terms of their low antigenicity. The human antibodies can be prepared by immunizing a mouse whose immune system is replaced with that of human (e.g., see "Functional transplant of megabase human immunoglobulin loci recapitulates human antibody response in mice" Mendez, M.J. et al. (1997) Nat. Genet. 15: 146-156). The humanized antibodies can be prepared by recombination of the hypervariable region of a monoclonal antibody (Methods in Enzymology (1991) 203: 99-121).

[0062] The use of the amino acid sequences of the polypeptides encoded by the cDNAs of the present invention enables predicting that the polypeptides have the following functions. It can be predict, from the results of homology

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search of SwissProt, GenBank, UniGene, or nr, that these polypeptides have such functions. Specifically, for instance, as shown in Examples, searching for a known gene or polypeptide that is homologous to the partial sequence of the full-length cDNA of the invention (1639 clone) and referring the function of the gene and of the polypeptide encoded by the gene make it possible to predict the function of the polypeptide encoded by the cDNA of the invention. In this way, each of 892 clones out of the 1639 full-length cDNA clones of the invention was predicted to encode a polypeptide that was classified into the following categories.

Secretory and/or membrane protein (439 clones)
 Glycoprotein-related protein (87 clones)
 Signal transduction-related protein (46 clones)
 Transcription-related protein (140 clones)
 Disease-related protein (219 clones)
 Enzyme and/or metabolism-related protein (168 clones)
 Cell division- and/or cell proliferation-related protein (23 clones)
 Cytoskeleton-related protein (60 clones)
 Nuclear protein and/or RNA synthesis-related protein (59 clones)
 Protein synthesis- and/or transport-related protein (24 clones)
 Cellular defense-related protein (6 clones)
 Development and/or differentiation-related protein (19 clones)
 DNA- and/or RNA-binding protein (158 clones)
 ATP- and/or GTP-binding protein (63 clones)

[0063] The functions of the polypeptides encoded by the cDNAs of the present invention can be predicted by assessing the presence of signal sequence, transmembrane region, nuclear translocation signal, glycosylation signal, phosphorylation site, and zinc finger motif, SH3 domain, etc. in the amino acid sequences. The programs, PSORT (Nakai K., and Kanehisa M. (1992) Genomics 14: 897-911), SOSUI (Hirokawa T. et al. (1998) Bioinformatics 14: 378-379) (Mitsui Knowledge Industry), and MEMSAT (Jones D.T., Taylor W.R., and Thornton J.M. (1994) Biochemistry 33: 3038-3049) can be used to predict the existence of the signal sequence or transmembrane region. Alternatively, a partial amino acid sequence of the polypeptide is fused with another polypeptide such as GFP, the fusion polypeptide is transfected into cultured cells, and the localization is analyzed to predict the function of the original polypeptide.

[0064] Based on the determined nucleotide sequences of the full-length cDNAs obtained in the present invention, it is possible to predict more detailed functions of the polypeptides encoded by the cDNA clones, for example, by searching the databases such as GenBank, Swiss-Prot, UniGene, and nr for homologies of the cDNAs; or by searching the amino acid sequences deduced from the full-length cDNAs for signal sequences by using software programs such as PSORT, for transmembrane regions by using software programs such as SOSUI or for motifs by using software programs such as Pfam (<http://www.sanger.ac.uk/Software/Pfam/index.shtml>) and PROSITE (<http://www.expasy.ch/prosite/>). As a matter of course, the functions are often predictable by using partial sequence information (preferably 300 nucleotides or more) instead of the full-length nucleotide sequences. However, the result of the prediction by using partial nucleotide sequence does not always agree with the result obtained by using full-length nucleotide sequence, and thus, it is needless to say that the prediction of function is preferably performed based on the full-length nucleotide sequences.

[0065] GenBank, Swiss-Prot, UniGene and nr databases were searched for homologies of the full-length nucleotide sequences of the 1639 clones (see Example 6). The amino acid sequences deduced from the full-length nucleotide sequences were searched for functional domains by PSORT, SOSUI and Pfam. Prediction of functions of polypeptides encoded by the clones and the categorization thereof were performed based on these results obtained. The categorization was carried out by the following method.

[1] Firstly, the cDNA clones were classified into the above-mentioned 14 functional categories based on the results of annotation-based categorization (using the keywords in the case of Swiss-Prot hit data; using Definition or Reference information in the case of GenBank, UniGene, or nr hit data), and the signal sequence search of the deduced ORFs by PSORT and the transmembrane region search by SOSUI.

[2] Secondly, clones which had been unassignable to the categories by the method of [1] were searched for functional domains and/or motifs by Pfam. Based on the results, the clones were additionally classified into the above-mentioned 14 types of categories when they had a functional domain and/or motif assignable to any one of the categories.

[0066] The following 439 clones presumably belong to secretory and/or membrane proteins.
 3NB6910000180, 3NB6910000850, 3NB6920000290, 3NB6920003300, 3NB6920005450, 3NB6920010020,

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ADRGL10000180, ADRGL10001600, ADRGL20003230, BGGI120010970, BNGH410000340, BNGH410001040,
 BNGH410001180, BNGH410001370, BNGH410001980, BRACE10000730, BRACE10001690, BRACE20002800,
 BRACE20007180, BRACE20010650, BRACE20011170, BRACE20011430, BRACE20013400, BRACE20013520,
 BRACE20014230, BRACE20014530, BRACE20014920, BRACE20015080, BRACE20018590, BRACE20022270,
 5 BRACE20024680, BRACE20026350, BRACE20026850, BRACE20030780, BRACE20031100, BRACE20034490,
 BRACE20071380, BRACE20071970, BRACE20072810, BRACE20074010, BRACE20074470, BRACE20075020,
 BRACE20075380, BRACE20076410, BRACE20076630, BRACE20076850, BRACE20077610, BRACE20077640,
 BRACE20077980, BRACE20078680, BRACE20079530, BRACE20084430, BRACE20086550, BRACE20089600,
 BRACE20091880, BRAWH10000010, BRAWH10000370, BRAWH10000940, BRAWH10001620, BRAWH10001800,
 10 BRAWH20001090, BRAWH20004430, BRAWH20006970, BRAWH20009840, BRAWH20011290, BRAWH20011410,
 BRAWH20011660, BRAWH20014380, BRAWH20014840, BRAWH20015030, BRAWH20036930, BRAWH20038320,
 BRAWH20040950, BRAWH20052250, BRAWH20059980, BRAWH20087060, BRAWH20092610, CD34C20000510,
 CTONG20013660, CTONG20015330, CTONG20028160, CTONG20037820, CTONG20047160, DFNES20003350,
 FCBBF10006180, FCBBF10006750, FCBBF20005910, FCBBF20007330, FCBBF20008150, FCBBF200094
 15 FCBBF20015380, FEBRA20003780, FEBRA20004040, FEBRA20004150, FEBRA20004520, FEBRA20004910,
 FEBRA20006560, FEBRA20006990, FEBRA20007330, FEBRA20008090, FEBRA20008800, FEBRA20010930,
 FEBRA20012270, FEBRA20012450, FEBRA20012940, FEBRA20013510, FEBRA20014870, FEBRA20014920,
 FEBRA20015840, FEBRA20020860, FEBRA20021910, FEBRA20025250, FEBRA20031550, FEBRA20037070,
 FEBRA20041100, FEBRA20041910, FEBRA20057780, FEBRA20063150, FEBRA20066670, FEBRA20067930,
 20 HCASM10000610, HCASM20002020, HEART20000990, HEART20004920, HHDP20000590, HLUNG10000240,
 HLUNG10000370, HLUNG10001100, HLUNG20001160, HLYRGA20001250, HLUNG20001420, HLUNG20001760,
 HLUNG20002550, HSYRA20003470, HSYRA20006290, HSYRA20008280, HSYRA20011030, HSYRA20013320,
 HSYRA20014200, HSYRA20015800, IMR3210000440, IMR3210001580, IMR3210002660, IMR3220007750,
 IMR3220008590, IMR3220009840, IMR3220014350, KIDNE10000080, KIDNE10001040, KIDNE10001430,
 25 KIDNE20000700, KIDNE20000850, KIDNE200016 KIDNE20003150, KIDNE20003310, KIDNE20003490,
 KIDNE20004220, KIDNE20005170, KIDNE20005190, KIDNE20033050, KIDNE20033570, KIDNE20039410,
 KIDNE20042620, KIDNE20042950, KIDNE20044110, KIDNE20048280, KIDNE20049810, KIDNE20054000,
 KIDNE20054770, KIDNE20060530, KIDNE20060620, KIDNE20063530, KIDNE20063760, KIDNE20066520,
 KIDNE20067600, KIDNE20071860, KIDNE20073520, KIDNE20074220, KIDNE20075690, LIVER10000580,
 30 LIVER10000670, LIVER10001040, LIVER10001110, LIVER10001750, LIVER10005420, LIVER20004160,
 MAMGL10000320, MAMGL10001840, MESAN10000350, MESAN10001470, MESAN10001800, MESAN20001490,
 NB9N420000420, NHNP200002060, NT2NE10000230, NT2NE10000830, NT2NE10001630, NT2NE20003270,
 NT2NE20003920, NT2NE20004550, NT2NE20004700, NT2NE20005500, NT2NE20012470, NT2NE20014350,
 NT2NE20016260, NT2NE20034080, NT2NE20047160, NT2NE20055170, NT2NE20057200, NT2RI20005970,
 35 NT2RI20009740, NT2RI20010100, NT2RI20014490, NT2RI20015400, NT2RI20015950, NT2RI20016570,
 NT2RI20018660, NT2RI20020220, NT2RI20021520, NT2RI20022430, NT2RI20022520, NT2RI20025300,
 NT2RI20030110, NT2RI20030510, NT2RI20031540, NT2RI20033010, NT2RI20033830, NT2RI20036730,
 NT2RI20042840, NT2RI20044420, NT2RI20049850, NT2RI20050870, NT2RI20051500, NT2RI20066820,
 NT2RI20068250, NT2RI20070480, NT2RI20070480, NT2RI20073030, NT2RI20074980, NT2RI20077540,
 40 NT2RI20078270, NT2RI20080500, NT2RI20081880, NT2RI20084810, NT2RI20085980, NT2RI20089420,
 NT2RI20092890, NT2RI20094060, NT2RP60000320, NT2RP60000390, NT2RP60001090, NT2RP70000690,
 NT2RP70002380, NT2RP70002590, NT2RP70003640, NT2RP70011660, NT2RP70015910, NT2RP70021510,
 NT2RP70023760, NT2RP70023790, NT2RP70026190, NT2RP70029820, NT2RP70040800, NT2RP70043730,
 NT2RP70047900, NT2RP70049250, NT2RP70055200, NT2RP70064080, NT2RP70071540, NT2RP70071770,
 45 NT2RP70073810, NT2RP70074220, NT2RP70075040, NT2RP70076170, NT2RP70079250, NT2RP70079750,
 NT2RP70081330, NT2RP70081370, NT2RP70083150, NT2RP70085500, NT2RP70090120, NT2RP70091490,
 NT2RP70091680, NT2RP70092360, NT2RP70093220, NT2RP70093730, NT2RP70094290, NT2RP70094810,
 NT2RP70094980, NT2RP70095070, NTONG10000980, NTONG10002140, NTONG10002570, NTONG20002650,
 NTONG20004290, NTONG20000200, NTONG20012220, OCBBF10000420, OCBBF20002310, OCBBF20009980,
 50 OCBBF20011210, PANCRI10000810, PLACE50000670, PLACE50000680, PLACE50001050, PLACE50001130,
 PLACE60012810, PLACE60018860, PLACE60020160, PLACE60020840, PLACE60026990, PLACE60037050,
 PLACE60037450, PLACE60043960, PLACE60044540, PLACE60047380, PLACE60049930, PLACE60050290,
 PROST10002200, PROST10002720, PROST10005260, PROST10005360, PROST12000360, PROST120026820,
 PROST20029600, PROST20032320, PROST20033020, PROST20039220, PROST20044160, PROST20051430,
 55 PROST20054260, PROST20056880, PROST20059190, PROST20059430, PROST20069880, PROST20072370,
 PROST20073890, PUAEIN10000570, PUAEIN10003220, SALGL10001570, SKMUS20007740, SKNMCI10000190,
 SKNMCI10000290, SKNMCI10002290, SKNMCI10002510, SKNMCI20011130, SKNMCI20015030, SMINT10000160,
 SMINT10000 SMINT10000570, SMINT10001180, SMINT20000180, SMINT20002770, SPLEN10000910,

	SPLN20001340,	SPLN200002430,	SPLN200002700,	SPLN200003100,	SPLN200004960,	STOMA10000520
	STOMA10001170,	STOMA200003020,	STOMA200002570,	SYNOV20001770,	SYNOV20016480,	TEST110000420
	TEST110000960,	TEST110001270,	TEST110001380,	TEST120001770,	TEST120008000,	TEST120007620,
5	TEST120008830,	TEST120009090,	TEST120009700,	TEST120011340,	TEST120012370,	TEST120013520,
	TEST120014200,	TEST120016210,	TEST120016710,	TEST120018520,	TEST120018620,	TEST120020020,
	TEST120020810,	TEST120022510,	TEST120024230,	TEST120024650,	TEST120024670,	TEST120025800,
	TEST120026320,	TEST120026960,	TEST120027000,	TEST120027070,	TEST120028660,	TEST120030370,
	TEST12003193,	TEST120034190,	TEST120036490,	TEST120039960,	TEST120042870,	TEST120047120,
	TEST120049940,	TEST120056900,	TEST120057420,	TEST120058600,	TEST120067740,	TEST120069780,
10	TEST120074800,	TEST120077490,	TEST120079510,	TEST120080200,	TEST120081440,	TEST120087740,
	TEST120086470,	TEST120136910,	THYMU10000830,	THYMU10001760,	THYMU10003290,	THYMU10003820,
	THYMU10005580,	TRACH10000630,	TRACH100011000,	TRACH10001400,	TRACH20001850,	TRACH20001960,
	TRACH20004020,	TRACH200004960,	TRACH200006650,	TRACH20007670,	TRACH20008980,	TRACH20015920,
	UMVEN20001330,	UTERU10000770,	UTERU10000960,	UTERU10001920,	UTERU20000470,	UTERU20003930,

[0067] The following 87 clones presumably belong to glycoprotein-related proteins.

	BNGH41000340	BNG410001180	BRACE20014920	BRACE20015080	BRACE20018590	BRACE20024680
	BRACE20026350	BRACE20031100	BRACE20074470	BRAWH10000370	BRAWH20001090	BRAWH20011660
	BRAWH20014840	BRAWH20059800	CD34C20000510	CTONG20013860	CTONG20028160	CTONG20037820
20	CFBB200700730	FEBRA200707330	FEBRA20080880	FEBRA20014920	FEBRA20015840	FEBRA20057780
	HEART2005060	HLUNG10001100	HLUNG20002550	HSYRA20013320	IMR321000680	IMR3220007750
	IMR3220013320	KIDNE20044110	KIDNE20063760	KIDNE20067600	KIDNE20073520	LIVER20000370
	MESAN10000350	NT2NE10000830	NT2NE10010850	NT2NE20003270	NT2NE20016260	NT2RI20018660
	NT2RI20025300	NT2RI20038780	NT2RI20077540	NT2RI20080500	NT2RI20085980	NT2RI20089420
25	NT2RI20092890	NT2RP70000690	NT2RP70004700	NT2RP70055200	NT2RP70081370	NT2RP70083150
	NT2RP70091490	NT2RP70092360	NT2RP70094980	NTONG10002140	OCBBF20002310	OCBBF20002770
	PLACE50000860	PLACE50001130	PLACE60018860	PLACE60044540	PROST20018230	PROST20032320
	PROST20073890	SALGL10001570	SKNMC20015030	SMINT10000160	SMINT20002770	SPLN20001340
	TEST110001270	TEST110001380	TEST120001770	TEST120024230	TEST120027070	TEST120036490
30	TEST120039980	TEST120056900	TEST120057420	TEST120079510	THYMU10001760	TRACH10000740
	TRACH10001250	TRACH20004200	UTERU20000470			

[0068] The following 46 clones presumably belong to signal transduction-related proteins.

35	ADRLG20000740	ASTR010000180	BRACE200055770	BRACE20022020	BRACE20027360	BRACE20027920
	BRAWH20006860	CTONG20005890	FEBRA200003350	HDPCC20005050	IMR3220003020	KIDNE20007300
	KIDNE20004840	KIDNE200053360	KIDNE200062990	NTR2R120033440	NTR2R120058110	NTR2R120062100
	NTR2R120073840	NTR2P70006240	NTR2P70043960	NTR2R70046870	NTR2P70061880	NTR2P70072520
	NTR2P70081440	NTR2P70093700	NTONG10018280	PBLM200004790	PLACE60026680	PROST20003940
40	PROST20043320	SKMUS10000220	SKMUS20016680	SPLN200003570	TEST120001540	TEST120005100
	TEST12002560	TEST120024680	TEST120029120	TEST120034980	TEST120049820	TEST120055840
	THYMU10003590	THYMU20003690	TRACH20002500	TRACH20002890		

[0069] The following 140 clones presumably belong to transcription-related proteins.

	3NB6920010220,	3NB120015110,	3NB6920015570,	ADRLG10000650,	BGGI120006480,	BGGI120006930,
	BGGI120017140,	BNGH41000080,	BNGH420005320,	BRACE10000930,	BRACE20014550,	BRACE20018550,
	BRACE20020910,	BRACE20024090,	BRACE20017140,	BRAWH10000020,	BRAWH10001640,	BRAWH10001880,
45	BRAWH20006330,	BRAWH20009010,	CTONG20025580,	CTONG20028200,	FCBBF10005980,	FCBBF20006940,
	FCBBF20009510,	FCBBF50002610,	FEBRA20003970,	FEBRA20004540,	FEBRA20004450,	FEBRA20009720,
	FEBRA20011460,	FEBRA20017150,	FEBRA20050140,	FEBRA20064760,	FEBRA20067360,	FEBRA20069420,
	FEBRA20072800,	HLUNG10000760,	HLUNG20000680,	HSYRA10001370,	HSYRA20016310,	IMR3210002420,
	IMR3220007420,	KIDNE20000510,	KIDNE20039940,	KIDNE20061490,	KIDNE20078110,	NESOP10000870,
50	NHNPC10001240,	NHNPC20002120,	NT2NE20002590,	NT2NE20008090,	NT2RI20003410,	NT2RI20004120,
	NT2RI20042410,	NT2RI20010830,	NT2RI20018460,	NT2RI20025410,	NT2RI20025550,	NT2RI20060710,
	NT2RI20067350,	NT2RI20071330,	NT2RI20074390,	NT2RI20078790,	NT2RI200871740,	NT2RI20090650,
	NT2RI20092150,	NT2RP60001000,	NT2RP60001270,	NT2RP70002710,	NT2RP70008120,	NT2RP70018560,
	NT2RP70024500,	NT2RP70032030,	NT2RP70038290,	NT2RP70042040,	NT2RP70045410,	NT2RP70045680,
55	NT2RP70055130,	NT2RP70061620,	NT2RP70062890,	NT2RP70064900,	NT2RP70068980,	NT2RP70075370,
	NT2RP70085570,	NT2RP70087200,	NT2RP70090190,	NTONG20003340,	NTONG20003630,	NTONG20015500,
	OCBBF20011010,	OCBBF20011240,	OCBBF20015860,	PEBLM20002450,	PEBLM20002700,	PEBLM20003080,
	PEBLM20003950,	PLACE60002050,	PLACE60005550,	PLACE60021510,	PLACE60030380,	PROST20018230,

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PROST20031170, PROST20073170, PUAEN10001610, SALGL10000650, SKMUS10000640, SKMUS20014920,
SKNMC20000650, SKNMC20002240, SKNMC20003560, SMINT10001000, SMINT20000540, SPLEN20000200,
SPLEN20000720, SYNNOV20010140, SYNNOV20013740, SYNNOV20014510, TEST110000550, TEST120001200,
TEST120007070, TEST120010490, TEST120015560, TEST120018150, TEST120018790, TEST120021490,
5 TEST120026760, TEST120027890, TEST120030710, TEST120034130, TEST120042290, TEST120053960,
TEST120074640, TEST120074660, TEST120078640, THYMU10004590, TRACH20000790, TRACH20002370,
TRACH20009440, UTERU10001600

[0070] The following 219 clones presumably belong to disease-related proteins.

ADRLG10000200, ADRLG10001600, ADRLG20000740, ASTRO20004170, BGGI120006840, BGGI120010970,
10 BGGI120017140, BNGH410001770, BNGH420005320, BRACE10001870, BRACE20006980, BRACE20007170,
BRACE20014550, BRACE20018550, BRACE20018590, BRACE20027550, BRACE20027720, BRACE20076850,
BRACE20086550, BRAWH10000020, BRAWH10001640, BRAWH20001770, BRAWH20005030, BRAWH20005220,
BRAWH20006630, BRAWH20006860, BRAWH20009840, BRAWH20011660, CD34C20000510, CTONG20005890,
CTONG20019110, CTONG20024180, CTONG20025580, CTONG20037820, CTONG20055530, FCBBF20000940,
15 FCBBF20009510, FCBBF40002820, FEBRA20001050, FEBRA20003990, FEBRA20004150, FEBRA20004540,
FEBRA20009720, FEBRA20010930, FEBRA20011460, FEBRA20050790, FEBRA20057880, FEBRA20064760,
FEBRA20067930, FEBRA20070170, FEBRA20075510, FEBRA20075660, HCASM200002140, HEART20004480,
HLUNG10001050, HLUNG20000680, HSYRA10001370, HSYRA20006400, HSYRA20013320, HSYRA20016310,
IMR3210000440, IMR3220007910, KIDNE10001040, KIDNE20003150, KIDNE20033730, KIDNE20042950,
20 KIDNE20044110, KIDNE20050420, KIDNE20059080, KIDNE20063760, KIDNE20078110, LIVER10002300,
LIVER10004330, LIVER20000330, LIVER20000370, MAMGL10001780, MESAN10001800, MESAN20002910,
MESAN20005010, NBN9410001350, NHNPC10000840, NHNPC20002120, NT2NE10000730, NT2NE20002990,
NT2NE20003690, NT2NE20005170, NT2NE20005360, NT2NE20006580, NT2NE20008090, NT2NE20013720,
NT2NE20016340, NT2NE20055170, NT2RI20004120, NT2RI20004210, NT2RI20010910, NT2RI20014500,
25 NT2RI20020410, NT2RI20029580, NT2RI20031540, NT2RI20033440, NT2RI20041900, NT2RI20056470,
NT2RI20057230, NT2RI20067030, NT2RI20070960, NT2RI20074980, NT2RI20077540, NT2RI20080500,
NT2RI20083960, NT2RI20084810, NT2RI20092150, NT2RI20092890, NT2RP60000350, NT2RP60001000,
NT2RP60001230, NT2RP70000690, NT2RP70044250, NT2RP70028750, NT2RP70029060, NT2RP70032030,
NT2RP70036290, NT2RP70042600, NT2RP70046560, NT2RP70049250, NT2RP70055020, NT2RP70062960,
30 NT2RP70063040, NT2RP70065270, NT2RP70069860, NT2RP70071770, NT2RP70073810, NT2RP70074220,
NT2RP70075370, NT2RP70079250, NT2RP70081440, NT2RP70090120, NT2RP70090190, NT2RP70093220,
NT2RP70094980, NTONG10002460, NTONG20003630, NTONG20015500, OCBBF10001180, OCBBF20008240,
PEBLM10000340, PEBLM20002480, PEBLM20003080, PEBLM20003950, PLAC200000800, PLAC20002050,
PLAC20003790, PLAC20014430, PROST10001670, PROST10005360, PROST20002730, PROST20032320,
35 PROST20033400, PROST20068200, PROST20072890, PROST20073890, PROST20085160, SALGL10001570,
SKMUS10000140, SKMUS10001180, SKMUS10001290, SKMUS20000740, SKMUS20003900, SKMUS20007240,
SKMUS20016340, SKNMC10002510, SKNMC20000650, SKNMC20003220, SMINT10000420, SMINT10000570,
SMINT10001000, SMINT10001030, SMINT20004000, SPLEN10001430, SPLEN20001970, STOMA20000880,
STOMA20003960, SYNNOV20013740, SYNNOV20014510, SYNNOV20016480, TEST110001270, TEST120001310,
40 TEST120001200, TEST120001770, TEST120002530, TEST120006000, TEST120006990, TEST120007620,
TEST120008830, TEST120011800, TEST120012690, TEST120015120, TEST120018520, TEST120018790,
TEST120021490, TEST120025160, TEST120027070, TEST120027290, TEST120029120, TEST120033250,
TEST120049820, TEST120053960, TEST120068660, TEST120071830, TEST120074640, TEST120079510,
TEST120086570, TEST120140360, THYMU10000830, THYMU10001760, THYMU10003590, THYMU10004910,
45 TRACH20002370, UTERU10000960, UTERU20000470

[0071] The following 168 clones presumably belong to the category of enzymes and/or metabolism-related proteins.

3NB6520002810, ADRLG10001600, ADRLG10001650, BGGI120005330, BNGH410000340, BNGH410001770,
BRACE10000420, BRACE20015080, BRACE20022020, BRACE20024680, BRACE20026850, BRACE20027360,
BRACE20027720, BRACE20027920, BRACE20071380, BRACE20084430, BRAWH20001770, BRAWH20006510,
50 BRAWH20006860, BRAWH20009840, BRAWH20011660, BRAWH20014180, BRAWH20014840, BRAWH20036890,
BRAWH20059880, BRAWH20069890, BRAWH20089560, CTONG20013660, CTONG20019110, DFNES20002120,
FCBBF20007330, FCBBF20015380, FEBRA20000350, FEBRA20001290, FEBRA20003110, FEBRA20024420,
FEBRA20041100, FEBRA20045920, FEBRA20050790, FEBRA20052160, FEBRA20062700, FEBRA20063150,
HEART20000350, HHDP20000550, HHDP20004450, HLUNG10001050, HLUNG20002550, HSYRA10001680,
55 HSYRA20005100, HSYRA20015740, IMR3220008380, IMR3220009190, IMR3220012180, IMR3220013170,
KIDNE20000410, KIDNE20003490, KIDNE20004220, KIDNE20005130, KIDNE20033050, KIDNE20040840,
KIDNE20044810, KIDNE20056290, KIDNE20060530, KIDNE20063760, KIDNE20068800, KIDNE20073280,
KIDNE20073520, KIDNE20078100, LIVER10000670, LIVER10002300, MAMGL10001780, MESAN20002910,

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MESAN20005010, NT2NE10000730, NT2NE10001850, NT2NE20002140, NT2NE20003270, NT2NE20003690, NT2NE20005860, NT2NE20013720, NT2NE20016340, NT2NE20016660, NT2RI10000480, NT2RI20010100, NT2RI20015400, NT2RI20020220, NT2RI20025300, NT2RI20033010, NT2RI20036780, NT2RI20037510, NT2RI20051500, NT2RI20068550, NT2RI20073840, NT2RI20074980, NT2RI20084810, NT2RI20087910, NT2RP70004770, NT2RP70006240, NT2RP70011660, NT2RP70026190, NT2RP70062960, NT2RP70072520, NT2RP70076100, NT2RP70081440, NT2RP70084060, NT2RP70085570, NT2RP70093700, NTONG10001820, OCBBF20008240, OCBBF20012 OCBBF20014080, OCBBF20014940, PANCRI10000210, PEBLM20004790, PLACE50001050, PLACE50001130, PLACE60003790, PLACE60012810, PLACE60018860, PLACE60044540, PROST20031170, PROST20032320, PROST20033400, PROST20051210, PROST20064500, SKMUS20001290, SKMUS10001770, SKMUS20000740, SKMUS20007240, SKMUS20008630, SKMUS20009330, SKMUS20011290, SKNSH10001740, SKNSH20003470, SMINT10000160, SPLEN20000130, STOMA10001080, STOMA20001210, STOMA20004820, SYNOV20016480, TESTI10000700, TESTI10001380, TESTI20001540, TESTI20005910, TESTI20012690, TESTI20018270, TESTI20022560, TESTI20027070, TESTI20029120, TESTI20034190, TESTI20034980, TESTI20040000, TESTI20042070, TESTI20042950, TESTI20047120, TESTI20049620, TESTI20138320, TESTI20140360, TESTI30000020, THYMU10000830, THYMU10004910, THYMU20003170, THYMU20003690, TRACH20000150, TRACH20004720, TRACH20004970, THYMU20002260, UTERU10000960

[0072] The following 23 clones presumably belong to the category of cell division- and/or cell proliferation-related proteins.

BGGI120001610, BRACE20027550, BRACE20076850, BRAWH20005030, BRAWH20005220, FEBRA20075660, HCASM20002140, HLUNG10000640, IMR3220009730, NT2NE20003840, NT2RI20006850, NT2RI20004190, NT2RI20058110, NTONG10002460, NTONG20008780, SKMUS20016340, SKNMC20003220, SPLEN10001430, TESTI10001680, TESTI20001840, TESTI20021050, TESTI20035120, TESTI20057310

[0073] The following 80 clones presumably belong to the category of cytoskeleton-related proteins.

ADRL10000020, BRACE20006980, BRACE20008850, BRACE20027960, BRACE20074470, BRACE20076630, BRACE20078820, BRACE20093070, BRAWH20000480, BRAWH200066220, CTONG20019550, CTONG20028160, CTONG20055530, DFNES20002680, FCBBF20005910, FEBRA20007720, FEBRA20008810, FEBRA20034290, FEBRA20043290, FEBRA20072000, HEART20004480, HEART20005200, HLUNG10001100, HSYRA20006050, IMR3220007910, KIDNE200040840, KIDNE20052960, NT2RI20014090, NT2RI20032220, NT2RI20058510, NT2RI20090860, NT2RP70000690, NT2RP70004250, NT2RP70028700, NT2RP70042600, NT2RP70049250, NT2RP70074220, NTONG20009660, OCBBF20011760, OCBBF20015280, PEBLM10000680, PROST10001670, PROST20033380, TESTI10000420, TESTI10000510, TESTI20003560, TESTI20004350, TESTI20008000, TESTI20006990, TESTI20008490, TESTI20008830, TESTI20011410, TESTI20015110, TESTI20016610, TESTI20020570, TESTI20024230, TESTI20031090, TESTI20031170, TESTI20039140, TESTI20078720

[0074] The following 59 clones presumably belong to the category of nuclear proteins and/or RNA synthesis-related proteins.

3NB6920002810, 3NB6920015280, BGGI120005440, BRACE10001150, BRACE20024780, BRACE20027550, BRAWH20005030, BRAWH20014180, BRAWH20069890, CTONG20024180, FEBRA20001290, FEBRA20075660, HEART20003090, HLUNG10000640, HSYRA10001680, HSYRA20005100, IMR3220008630, IMR3220012180, MAMGL10001780, NT2NE10001850, NT2NE20002140, NT2NE20003840, NT2RI20016660, NT2NE20054410, NT2RI20002820, NT2RI20006850, NT2RI20010910, NT2RI20025540, NT2RI20041900, NT2RI20053350, NT2RI20057230, NT2RI20060720, NT2RI20067030, NT2RI20068550, NT2RI20077840, NT2RI20087490, NT2RP70004770, NT2RP70013060, NT2RP70076430, NTONG20008780, PEBLM10000340, PLACE50000580, PLACE60003790, PROST20001760, PROST20062600, SKMUS20016340, SKMUS20016340, SKNMC20003220, SPLEN10001430, SPLEN20001970, TESTI10001680, TESTI20002530, TESTI20007840, TESTI20021050, TESTI20029120, TESTI20035120, TESTI20057310, TRACH20003930, TRACH20012890

[0075] The following 24 clones presumably belong to the category of protein synthesis- and/or protein transport-related proteins.

BRACE20078880, FEBRA20075510, IMR3220008380, KIDNE20005190, KIDNE20050420, MESAN20002910, NB9NA10001350, NT2NE20005360, NT2RI20032050, NT2RI20032220, NT2RP70000760, NT2RP70076430, NT2RP70083940, OCBBF20008240, PLACE50000580, PROST20005030, SKMUS20000740, SKMUS20008630, TESTI20007840, TESTI20015120, TESTI20018690, TESTI20078720, THYMU10005580, UMVEN20001330

[0076] The following 6 clones presumably belong to the category of cellular defense-related proteins.

BRACE20014550, NT2RI20037510, NT2RI20053350, NT2RP70029060, NT2RP70062960, PLACE50001700

[0077] The following 19 clones presumably belong to the category of development and/or differentiation-related proteins.

BGGI120006930, CTONG20028200, FCBBF50002610, FEBRA20014920, FEBRA20017150, FEBRA20060920, MAMGL10001820, NESOP10000870, NHNPC10001240, NT2RI20078790, NT2RP70008120, NT2RP70018560, NT2RP70045410, OCBBF20002770, SALGL10000650, SMINT10001000, TESTI10000550, TESTI20026760

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TESTI20078140

[0078] The following 158 clones presumably belong to the category of DNA- and/or RNA-binding proteins.

3NB6920002810, 3NB6920010220, 3NB6920015110, 3NB6920015570, ADRGL10000650, BGGI120006840, BGGI120006930, BNGH410000800, BNGH420005320, BRACE20014550, BRACE20020910, BRACE20024090, BRACE20024780, BRACE20071740, BRAWH10001640, BRAWH10001680, BRAWH20000340, BRAWH20006330, BRAWH20009010, BRAWH20014180, BRAWH20069890, CTONG20025580, CTONG20028200, D3OST20001840, FCBBF10005980, FCBBF20009510, FCBBF50002610, FEBRA20003970, FEBRA20003990, FEBRA20004540, FEBRA20008560, FEBRA20009720, FEBRA20017150, FEBRA20017900, FEBRA20050140, FEBRA20064760, FEBRA20067360, FEBRA20072800, HEART20003090, HLUNG10000760, HSYRA10001370, HSYRA20016310, IMR3210002420, IMR3220007420, IMR3220008630, KIDNE20000510, KIDNE20039940, KIDNE20061490, KIDNE20078110, NESOP10000870, NHNPC10000840, NHNPC10001240, NHNPC20002120, NT2NE20002590, NT2NE20003840, NT2NE20008090, NT2NE20016660, NT2NE20054410, NT2RI20003410, NT2RI20004210, NT2RI20006850, NT2RI20010830, NT2RI20010910, NT2RI20025410, NT2RI20025850, NT2RI20057230, NT2RI20060710, NT2RI20067350, NT2RI20071330, NT2RI20074390, NT2RI20078790, NT2RI20078840, NT2RI20087140, NT2RI20087490, NT2RI20090650, NT2RP60001000, NT2RP60001270, NT2RP70002710, NT2RP70008120, NT2RP70013060, NT2RP70018560, NT2RP70024500, NT2RP70032030, NT2RP70042040, NT2RP70045410, NT2RP70046560, NT2RP70055130, NT2RP70061620, NT2RP70062960, NT2RP70064900, NT2RP70069860, NT2RP70075370, NT2RP70085170, NT2RP70085750, NT2RP70087200, NT2RP70090190, NTONG20003340, NTONG20008780, NTONG20015500, OCBBF20011010, OCBBF20015860, PEBLM10000340, PEBLM20001120, PEBLM20002700, PEBLM20003080, PEBLM20003080, PLACE60000250, PLACE60005550, PLACE60021510, PLACE60030380, PROST20001760, PROST20003250, PROST20018230, PROST20031170, PROST20026020, PROST20073170, SALGL10000650, SKMUS10000640, SKMUS20014920, SKMUS20016340, SKNMC20000650, SKNMC20002240, SKNMC20003220, SKNMC20003560, SMINT10001000, SMINT20005450, SPLEN10001430, SPLEN20000200, SPLEN20000720, SPLEN20001970, SYNOV20010140, SYNOV20013740, SYNOV20014510, TESTI20000550, TESTI20001200, TESTI20007070, TESTI20010490, TESTI20013450, TESTI20015560, TESTI20018150, TESTI20021050, TESTI20021490, TESTI20026760, TESTI20027890, TESTI20030710, TESTI20033270, TESTI20034130, TESTI20053960, TESTI20074640, TESTI20074660, TESTI20078640, THYMU10004590, TRACH20000790, TRACH20002370, TRACH20009440, TRACH20012890, UTERU10001600

[0079] The following 63 clones presumably belong to the category of ATP- and/or GTP-binding proteins.

3NB6920002810, BNGH410000390, BRACE20022020, BRACE20028120, BRACE20071380, BRAWH20000480, BRAWH20006860, BRAWH20006620, CTONG20013200, DFNES20002680, FEBRA20043290, FEBRA20052160, FEBRA20072000, FEBRA20075510, HHDP200000550, HLUNG20001160, HSYRA10001680, HSYRA20000510, HSYRA20006050, KIDNE200040840, MAMGL10001780, MESAN20002910, NB9N410001350, NT2NE20003690, NT2NE20005170, NT2NE20016660, NT2NE20055170, NT2RI20006850, NT2RI20073840, NT2RP70004290, NT2RP70011660, NT2RP70029060, NT2RP70036290, NT2RP70042600, NT2RP70046870, NT2RP70062560, NT2RP70081370, NT2RP70081440, NT2RP70093700, OCBBF20008240, OCBBF20015280, PEBLM20004790, PLACE50001700, PLACE60003790, PROST20018990, PROST20033400, SKMUS20008030, SMINT10000420, TESTI20001540, TESTI20003560, TESTI20005910, TESTI20006950, TESTI20006990, TESTI20084990, TESTI20015110, TESTI20016610, TESTI20022560, TESTI20029120, TESTI20034980, TESTI20042290, TESTI20047120, TESTI20049820, TESTI20057310

[0080] Among the clones other than the ones shown above, NTONG10001300 is a clone which was predicted to highly possibly belong to the category of secretory protein and/or membrane protein based on the result of domain search by Pfam.

FEBRA20017060, NT2RI20066790, SMINT10000710

[0081] The three clones shown above are clones which were predicted to highly possibly belong to the category of glycoprotein-related protein based on the result of domain search by Pfam.

BRACE20080970, BRACE20092120, BRAWH10001300, FEBRA20019890, KIDNE20031850, KIDNE20060140, MESAN20000920, NB9N410000470, NT2RI20071480, NT2RI20078910, NT2RP70088550, NTONG20016120, OCBBF10000910, PROST20094830, SKNSH10003010, SPLEN20002670, TESTI20031960, TESTI20036250, TESTI20037810, TESTI20083870, TESTI20177400

[0082] The 21 clones shown above are clones which were predicted to highly possibly belong to the category of signal transduction-related protein based on the result of domain search by Pfam.

3NB6920009120, 3NB6920014710, FEBRA10001660, FEBRA20083850, BRAWH20004760, BRAWH20012030, CTONG20011390, CTONG20018200, FEBRA20007870, FEBRA20043250, HHDP20003150, NT2RI10000270, NT2RI20036950, NT2RI20053680, NT2RI20072540, NT2RI20083360, NT2RP70030550, OCBBF20013070, OCBBF20015270, PLACE60046630, PROST10003430, PROST20067370, SKMUS10001040, SKNMC20015960, TESTI20030050, TESTI20033540, TESTI20035890, TESTI20068720, TRACH20004110

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[0083] The 29 clones shown above are clones which were predicted to highly possibly belong to the category of transcription-related protein based on the result of domain search by Pfam.

BNGH410001900, BRACE20080970, BRACE20092120, BRAWH20093600, FEBRA20003770, FEBRA20024290, HLUNG10000990, KIDNE20004030, MESAN20000920, NB9N420001040, NT2NE10000140, NT2NE20001740, NT2RI200050610, NT2RI200055640, NT2RI20072540, NT2RI20074690, NT2RP60000860, NT2RP70036470, NT2RP70036800, NT2RP70072210, NT2RP70074060, NT2RP70084870, NTONG10001300, NTONG10002640, NTONG20016120, OCBBF10000910, OCBBF10001190, OCBBF20007190, SKMUS20001170, SKMUS20016620, SKNMC20000970, SKNMC20015960, SYNOV10001280, TEST120002380, TEST120006270, TEST120013300, TEST12001520, TEST120036250, TEST120037810, TEST120064830, TEST120083870, TRACH20006750, TRACH20016070

[0084] The 43 clones shown above are clones which were predicted to highly possibly belong to the category of enzyme and/or metabolism-related protein based on the result of domain search by Pfam.

NT2RI20064120

[0085] The 1 clone shown above is a clone which was predicted to highly possibly belong to the category of cell division and/or cell proliferation-related protein based on the result of domain search by Pfam.

BRACE20083800, KIDNE20004970

[0086] The 2 clones shown above are clones which were predicted to highly possibly belong to the category of cytoskeleton-related protein based on the result of domain search by Pfam.

3NB6920009120, 3NB6920014710, BRACE10001660, BRACE20083850, BRAWH20004760, BRAWH20012030, BRAWH20064500, CTONG20011390, CTONG20018200, FEBRA20007870, FEBRA20043250, HCASM20003070, HDPDC20003150, NT2RI10000270, NT2RI20036950, NT2RI20053680, NT2RI20072540, NT2RI20083360, NT2RP70012310, NT2RP70030550, NT2RP70036470, OCBBF20013070, OCBBF20015270, PLACE60046630, PROST10003430, PROST20067370, SKMUS10001040, SKNMC20000970, SKNMC20015960, TEST120030050, TEST120032280, TEST120033540, TEST120035890, TEST120068720, TRACH20004110

[0087] The 34 clones shown above are clones which were predicted to highly possibly belong to the category of DNA- and/or RNA-binding protein based on the result of domain search by Pfam.

NT2RI20064120

[0088] The 1 clone shown above is a clone which was predicted to highly possibly belong to the category of ATP- and/or GTP-binding proteins based on the result of domain search by Pfam.

[0089] The 185 clones shown below are clones which were unassignable to any of the above-mentioned categories, but have been predicted to have some functions based on homology search using their full-length nucleotide sequences and motif search in their estimated ORFs.

3NB6910001160, ASTRO20004170, BNGH410000030, BNGH410001900, BRACE20005250, BRACE20014770, BRAWH20016730, BRACE20017370, BRACE20024310, BRACE20028960, BRACE20077840, BRACE20083850, BRAWH20004320, BRAWH20009440, BRAWH20076050, CTONG20018200, CTONG20027210, CTONG20064490, DFNES20004300, FCBBF10006870, FCBBF20002760, FCBBF20001210, FEBRA20000530, FEBRA20005360, FEBRA20007570, FEBRA20011330, FEBRA20019890, FEBRA20030540, FEBRA20043250, FEBRA20044900, FEBRA20048180, FEBRA20053800, FEBRA20068730, FEBRA20070170, HCASM10000210, HCASM20005360, HDPDC20001150, HDPDC20001490, HLUNG10000990, HSYRA10001190, HSYRA200001350, HSYRA20006400, IMR3220002230, IMR3220014910, KIDNE10001520, KIDNE20003750, KIDNE20004970, KIDNE20005740, KIDNE20031850, KIDNE20043440, KIDNE20056760, KIDNE20059080, KIDNE20060140, KIDNE20060300, KIDNE20067750, LIVER10000790, LIVER10004330, MESAN10001010, MESAN20000920, NB9N410000470, NB9N420001040, NB9N420004950, NT2NE10000180, NT2NE10000630, NT2NE20013370, NT2NE20016970, NT2NE20035690, NT2NE20053710, NT2RI200006890, NT2RI20013420, NT2RI20013850, NT2RI20015190, NT2RI20016210, NT2RI20022700, NT2RI20025170, NT2RI20029260, NT2RI20029580, NT2RI20043040, NT2RI20061830, NT2RI20064120, NT2RI20065060, NT2RI20074690, NT2RI20077230, NT2RI20082210, NT2RI20083960, NT2RI20088120, NT2RP60000080, NT2RP60000350, NT2RP60000720, NT2RP60000860, NT2RP70009060, NT2RP70010800, NT2RP70022430, NT2RP70028290, NT2RP70033040, NT2RP70036320, NT2RP70036800, NT2RP70042330, NT2RP70049150, NT2RP70052050, NT2RP70055020, NT2RP70063040, NT2RP70072210, NT2RP70084410, NT2RP70084870, NTONG10000520, NTONG10001230, NTONG10001300, OCBBF10001220, OCBBF20007190, OCBBF20011400, OCBBF20014020, OCBBF20014940, PEBLM10001440, PEBLM20002130, PLACE50000370, PLACE50000800, PLACE60014430, PLACE60024190, PLACE60033990, PLACE60038500, PLACE60043970, PLACE60044640, PROST20023380, PROST20034720, PROST20067370, PROST20079740, SALGL10000470, SKMUS10000140, SKMUS10001040, SKMUS10001180, SKMUS20001170, SKMUS20003650, SKMUS20003900, SKMUS20004580, SKMUS20009020, SKMUS20009540, SKMUS20010080, SKMUS20014750, SKMUS20015430, SKMUS20016820, SKNMC20000970, SKNMC20015960, SMINT10001030, SMINT20001450, SMINT20003960, SMINT20004000, SPLEN20002670, SYNOV10001280, SYNOV20002910, SYNOV20008200, TEST110000250, TEST110000640, TEST110001310, TEST110001910, TEST120000440,

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TESTI20002070, TESTI20002080, TESTI20014120, TESTI20016650, TESTI20022230, TESTI20022940,
 TESTI20024610, TESTI20027290, TESTI20030050, TESTI20030590, TESTI20030740, TESTI20035510,
 TESTI20035740, TESTI20041220, TESTI20052680, TESTI20054080, TESTI20064830, TESTI20065720,
 TESTI20068660, TESTI20071830, TESTI20078670, TESTI20083870, THYMU10000020, THYMU10002910,
 TRACH10000300, TRACH20006750, TRACH20007800, TRACH20008940, TRACH20013950

[0090] Further, the reason is that a polypeptide does not always belong solely to a single category of the above-described functional categories, and therefore, a polypeptide may belong to any of the predicted functional categories. Besides, additional functions can be found for the clones classified into these functional categories by further analyses.

[0091] Since the polypeptide encoded by clones of the invention contains full-length amino acid sequence, it is possible to analyze its biological activity, and its effect on cellular conditions such as cell proliferation and differentiation by expressing the polypeptide as a recombinant polypeptide using an appropriate expression system, injecting the recombinant into the cell, or raising a specific antibody against the polypeptide.

[0092] The biological activities of respective polypeptides can be analyzed by the methods as shown below.

Secretory protein, transmembrane protein:

"Ion Channels" (Ed., R. H. Ashley, 1995) of "The Practical Approach Series" (IRL PRESS),

"Growth Factors" (Eds., I. McKay, I. Leigh, 1993),

"Extracellular Matrix" (Eds., M. A. Haralson, J. R. Hassell, 1995);

Glycoprotein-related protein:

"Glycobiology" (Eds., M. Fukuda, A. Kobata, 1993) of "The Practical Approach Series" (IRL PRESS),

"Glycoprotein Analysis in Biomedicine" (Ed., Elizabeth F. Hounsell, 1993) of "Method in Molecular Biology" (Humana Press) series;

Signal transduction-related protein:

"Signal Transduction" (Ed., G. Milligan, 1992) of "The Practical Approach Series" (IRL PRESS),

"Protein Phosphorylation" (Ed., D. G. Hardie, 1993), or

"Signal Transduction Protocols" (Eds., David A. Kendall, Stephen J. Hill, 1995) of "Method in Molecular Biology" (Humana Press) series;

Transcription-related protein:

"Gene Transcription" (Eds., B. D. Hames, S. J. Higgins, 1993) of "The Practical Approach Series" (IRL PRESS),

"Transcription Factors" (Ed., D.S. Latchman, 1993);

Enzyme and/or metabolism-related protein:

"Enzyme Assays" (Eds., ROBERT EISENTHAL and MICHAEL J. DANSON, 1992) of "The Practical Approach Series" (IRL PRESS); Cell division and/or cell proliferation-related protein:

"Cell Growth, Differentiation and Senescence" (Ed., GEORGE STUDZINSKI, 2000) of "The Practical Approach Series" (IRL PRESS);

Cytoskeleton-related protein:

"Cytoskeleton: Signalling and Cell Regulation" (Eds., KERMIT L. CARRAWAY and CAROLIE A. CAROTHERS CARRAWAY, 2000) of "The Practical Approach Series" (IRL PRESS),

"Cytoskeleton Methods and Protocols" (Ed., Gavin, Ray H., 2000) of "Method in Molecular Biology" (Humana Press) series;

Nuclear protein and/or RNA synthesis-related protein:

"Nuclear Receptors" (Ed., DIDIER PICARD, 1999) of "The Practical Approach Series" (IRL PRESS),

"RNA Processing" (Eds., STEPHEN J. HIGGINS and B. DAVID HAMES, 1994);

Protein synthesis and/or transport-related protein:

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"Membrane Transport" (Ed., STEPHEN A. BALDWIN, 2000) of "The Practical Approach Series" (IRL PRESS),
 "Protein Synthesis Methods and Protocols" (Eds., Martin, Robin, 1998) of "Method in Molecular Biology" (Humana Press) series;

5 Cellular defense-related protein:

"DNA Repair Protocols" (Henderson, Daryl S., 1999) of "Method in Molecular Biology" (Humana Press) series,
 "Chaperonin Protocols" (Eds., Schneider, Christine, 2000);

10 Development and/or differentiation-related protein:

"Developmental Biology Protocols" (Eds., ROBERT EISENTHAL and MICHAEL J. DANSON, 1992) of "Method in Molecular Biology" (Humana Press) series;

15 DNA- and/or RNA-binding protein:

"DNA-Protein Interactions Principles and Protocols" (Eds., Kneale, G. Geoff, 1994) of "Method in Molecular Biology" (Humana Press) series,
 "RNA-Protein Interaction Protocols" (Eds., Haynes, Susan R., 1999);

20

ATP- and/or GTP-binding protein:

"Signal Transduction Protocols" (Eds., David A. Kendall, Stephen J. Hill, 1995) of "Method in Molecular Biology" (Humana Press) series.

25

[0093] In the categorization, the clone predicted to belong to the category of secretory and/or membrane protein means a clone having hit data with some annotation, such as growth factor, cytokine, hormone, signal, transmembrane, membrane, extracellular matrix, receptor, G-protein coupled receptor, ionic channel, voltage-gated channel, calcium channel, cell adhesion, collagen, connective tissue, etc., suggesting that it was a secretory or membrane protein, or a clone in which the presence of nucleotide sequence encoding a signal sequence or transmembrane region was suggested by the results of PSORT and SOSUI analyses for deduced ORF.

30

[0094] The clone predicted to belong to the category of glycoprotein-related protein means a clone having hit data with some annotation, such as glycoprotein, suggesting that the clone encodes a glycoprotein-related protein.

35

[0095] The clone predicted to belong to the category of signal transduction-related protein means a clone having hit data with some annotation, such as serine/threonine-protein kinase, tyrosine-protein kinase, SH3 domain, SH2 domain, etc., suggesting that the clone encodes a signal transduction-related protein.

[0096] The clone predicted to belong to the category of transcription-related protein means a clone having hit data with some annotation, such as transcription regulation, zinc finger, homeobox, etc., suggesting that the clone encodes a transcription-related protein.

40

[0097] The clone predicted to belong to the category of disease-related protein means a clone having hit data with some annotation, such as disease mutation, syndrome, etc., suggesting that the clone encodes a disease-related protein, or a clone whose full-length nucleotide sequence has hit data for Swiss-Prot, GenBank, UniGene, or nr, where the hit data corresponds to genes or polypeptides which have been deposited in the Online Mendelian Inheritance in Man (OMIM) (<http://www.ncbi.nlm.nih.gov/Omim/>), which is the human gene and disease database described later.

45

[0098] The clone predicted to belong to the category of enzyme and/or metabolism-related protein means a clone having hit data with some annotation, such as metabolism, oxidoreductase, E. C. No. (Enzyme commission number), etc., suggesting that the clone encodes an enzyme and/or metabolism-related protein.

[0099] The clone predicted to belong to the category of cell division and/or cell proliferation-related protein means a clone having hit data with some annotation, such as cell division, cell cycle, mitosis, chromosomal protein, cell growth, apoptosis, etc., suggesting that the clone encodes a cell division and/or cell proliferation-related protein.

50

[0100] The clone predicted to belong to the category of cytoskeleton-related protein means a clone having hit data with some annotation, such as structural protein, cytoskeleton, actin-binding, microtubules, etc., suggesting that the clone encodes a cytoskeleton-related protein.

[0101] The clone predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein means a clone having hit data with some annotation, such as nuclear protein, RNA splicing, RNA processing, RNA helicase, polyadenylation, etc., suggesting that the clone encodes a nuclear protein and/or RNA synthesis-related protein.

55

[0102] The clone predicted to belong to the category of protein synthesis and/or transport-related protein means a clone having hit data with some annotation, such as translation regulation, protein biosynthesis, amino-acid biosyn-

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thesis, ribosomal protein, protein transport, signal recognition particle, etc., suggesting that the clone encodes a protein synthesis and/or transport-related protein.

[0103] The clone predicted to belong to the category of cellular defense-related protein means a clone having hit data with some annotation, such as heat shock, DNA repair, DNA damage, etc., suggesting that the clone encodes a cellular defense-related protein.

[0104] The clone predicted to belong to the category of development and/or differentiation-related proteins means a clone having hit data with some annotation, such as developmental protein, etc., suggesting that the clone encodes a development and/or differentiation-related protein.

[0105] The clone predicted to belong to the category of DNA- and/or RNA-binding protein means a clone having hit data with some annotation, such as DNA-binding, RNA-binding, etc.

[0106] The clone predicted to belong to the category of ATP- and/or GTP-binding protein means a clone having hit data with some annotation, such as ATP-binding, GTP-binding, etc.

[0107] As to a protein involved in a disease, it is possible to perform a functional analysis as described above, but also possible to analyze correlation between the expression or the activity of the protein and a certain disease by using a specific antibody that is obtained by using expressed protein. Alternatively, it is possible to utilize the database OMIM, which is a database of human genes and diseases, to analyze the protein. Further, new information is constantly being deposited in the OMIM database. Therefore, it is possible for one skilled in the art to find a new relationship between a particular disease and a gene of the present invention in the most up-to-date database. The proteins involved in diseases are useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as a target of gene therapy.

[0108] Also, as for a secretory protein, membrane protein, signal transduction-related protein, glycoprotein-related protein, or transcription-related protein, etc., search of the OMIM with the following keywords resulted in the finding that the proteins are involved in many diseases (the result of the OMIM search for secrete and membrane proteins is shown below). Also, association between proteins related to signal transduction or transcription and diseases is reported in "Transcription Factor Research-1999" (Fuji, Tamura, Morohashi, Kageyama, and Satake edit, (1999) Jikken-gaku Zoukan, Vol.17, No.3), and "Gene Medicine" (1999) Vol.3, No.2). When cancer is used as an example, as described in "Biology of Cancer" (S. Matsubara, 1992) of Life Science series (Shokabo), many proteins are involved in cancers, which include enzyme and/or metabolism-related proteins, cytoskeleton-related proteins, cell division and/or cell proliferation-related proteins as well as secretory proteins, membrane proteins, signal transduction-related proteins, glycoprotein-related proteins, transcription-related proteins. As clearly seen by the above example, it is evident that not only disease-related proteins but also secretory proteins, membrane proteins, signal transduction-related proteins, glycoprotein-related proteins, transcription-related proteins, etc. are often involved in diseases, and thus they can be useful targets in the field of medical industry.

[0109] The result of the OMIM search for secretory and membrane proteins is shown below, in which the keywords,

- (1) secretion protein,
- (2) membrane protein,
- (3) channel, and
- (4) extracellular matrix were used.

[0110] Shown in the search result are only the accession numbers in the OMIM. Using the number, data showing the relationship between a disease and a gene or protein can be seen. The OMIM data has been renewed everyday

1) Secretion protein

354 entries found, searching for "secretion protein"

'604667, '104760, '176860, '151675, '139320, '107400, '604029, '118910, #200100, '176880, '603850, '147572, '604028, '179513, '125950, '139250, '246700, '600946, '600560, '602926, '185860, '605083, '603215, '602421, '157147, '179512, '600174, '109270, '604710, '138120, '179510, '600998, '179509, '170280, '179511, '600626, '603831, '601489, '154545, '179490, '603826, '122559, '603216, '102720, '147290, '164180, '603062, '112262, '602672, '605435, '605322, '131230, '601652, '603166, '601746, '601591, '179508, #160900, '104311, '600759, '147545, '167805, #104300, '167770, #219700, '168470, '601684, '602049, '601146, '605227, '602434, '602534, '114840, '603489, '604323, '107470, '600753, '600768, '118825, '600564, '604252, '173120, '134370, '192340, '308230, '600322, '605359, '600046, '300090, '106160, '600041, #262500, '605563, '150390, '158106, '182590, #103580, '104610, '173900, '134797, '143890, #145980, '306900, '308700, '176300, '227500, '137350, #154700, '138079, '600760, '107730, '142410, '147670, '124092, '590050, '152760, '600509, '605646, '201910, '227600, '152790, '300200, '300300, '300800, '138160, '107741, '120150, '601199, '120180, '120160, '176730, '133170,

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*122560, *107300, *137241, *120140, *101000, *193400, *217000, *272800, *600937, *201710, *600377, *174800, *106100, *274800, *173350, *177170, *147620, *214500, *131244, *202110, *120120, *601007, *191160, *147470, *603372, *600733, *252800, *190160, *138040, *158070, *162151, *125700, *130070, *113811, *603355, *171060, *136435, *184700, *603732, *190180, *164008, *186590, *120220, *604312, *152200, *138130, *605085, *605533, *600840, *166210, *188545, *207750, *173360, *601933, *194050, *153450, *138850, *253200, *307030, *157145, *600514, *600262, *264080, *147380, *600281, *204000, *227810, *232200, *188826, *232800, *161561, *166200, *188400, *153620, *182099, *218040, *265800, *172400, *177200, *176805, *211600, *214700, *176410, *152780, *600633, *601771, *301500, *605402, *601922, *307800, *147892, *147720, *312060, *602000, *147660, *106150, *602358, *107270, *601769, *147440, *604558, *131530, *600270, *601810, *603692, *603401, *600423, *601604, *603345, *125853, *602843, *142640, *603044, *605740, *134830, *602779, *130660, *139191, *137035, *600761, *601340, *600823, *107740, *130160, *600877, *605110, *600945, *130080, *600957, *130050, *605580, *118444, *601124, *124020, *122470, *120700, *603201, *137216, *601185, *138945, *218030, *600839, *240800, *262400, *162300, *162330, *188450, *265580, *126241, *300159, *601038, *191390, *201810, *601398, *602384, *131240, *602423, *139392, *142703, *602663, *232700, *602682, *602722, *602730, *600734, *188540, *182452, *601538, *603061, *146880, *603140, *603160, *142704, *252650, *182280, *125255, *603252, *131750, *182139, *182100, *259420, *261100, *603493, *601745, *182098, *603795, *123812, *600264, *147940, *180246, *180245, *118888, *604284, *168450, *118455, *604398, *604433, *601919, *184445, *600031, *604961, *605032, *605033, *171050, *171300, *131243, *109160, *605254, *274900, *171400, *600042, *151670, *184600, *605470, *605546, *176760, *602008, *102200, *605720, *600732, *605901

2) Membrane protein

1489 entries found, searching for "membrane protein"

*130500, *605704, *305360, *153330, *173610, *109270, *170995, *170993, *104776, *602333, *309060, *605703, *120920, *605943, *602690, *159430, *600897, *133090, *601178, *602413, *602003, *604405, *605940, *603237, *109820, *600378, *602173, *107776, *602334, *602335, *125305, *601134, *309845, *605731, *154045, *603241, *603718, *600594, *603214, *185881, *603657, *600182, *603177, *605331, *601476, *605456, *601114, *605190, *600723, *603904, *136950, *300222, *602879, *185880, *605348, *300096, *602257, *177070, *310200, *603062, *603344, *600039, *602977, *300100, *128240, *600959, *600322, *227400, *186945, *600946, *602534, *602048, *182900, *601097, *600267, *602625, *136430, *602421, *601047, *107450, *143450, *603141, *184756, *164730, *159440, *154050, *600579, *312080, *604202, *603700, *600447, *255540, *604691, *158343, *600403, *602414, *137290, *176640, *176981, *600179, *600754, *604456, *604693, *605675, *604605, *188860, *300172, *602910, *604323, *219800, *601848, *603179, *600279, *602251, *222700, *603831, *605072, *605377, *601028, *604155, *108733, *104225, *601896, *601510, *173335, *107770, *601767, *600046, *603850, *600040, *603784, *603234, *188560, *605863, *121015, *605862, *605861, *186946, *604252, *603215, *124681, *604597, *603143, *605264, *603735, *176860, *605536, *176801, *180721, *603355, *104760, *131560, *310300, *602631, *304700, *309400, *603142, *143890, *605431, *600753, *115501, *176790, *600266, *601691, *168468, *601239, *602216, *104300, *605613, *601595, *605550, *125950, *605475, *602217, *602261, *603534, *602262, *604631, *190315, *601313, *604306, *104311, *604672, *605600, *602461, *605548, *602296, *604376, *121014, *121011, *600691, *604262, *139310, *304040, *605445, *179514, *179512, *151480, *160900, *120130, *128239, *601158, *601403, *176943, *601014, *300800, *300294, *600175, *185470, *273800, *605034, *602887, *185000, *604871, *603593, *603583, *605454, *104775, *605872, *141180, *602713, *603531, *139150, *601531, *601832, *605452, *134651, *604156, *120620, *605883, *604142, *169645, *605324, *600816, *604699, *300112, *605182, *600164, *182180, *605071, *300023, *605057, *308240, *300249, *176947, *176894, *605081, *605035, *602044, *182860, *107271, *305100, *153390, *113730, *602689, *180069, *603518, *300017, *191275, *177061, *601693, *601789, *604241, *600934, *138160, *604424, *603868, *600174, *600718, *600523, *604141, *601009, *605251, *600481, *600874, *155550, *605227, *601017, *162230, *601138, *604157, *601212, *600763, *604110, *604158, *601107, *601326, *600621, *600587, *601137, *600917, *600855, *605058, *194355, *605194, *603291, *102720, *136425, *170715, *603216, *605547, *135630, *602926, *600168, *605002, *602474, *600157, *603025, *603893, *231200, *120090, *601966, *131230, *604722, *604721, *604515, *246700, *602101, *605628, *303630, *605787, *602857, *602285, *605708, *602488, *605025, *603817, *300051, *603293, *176878, *603646, *605707,

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3) Channel (member of membrane protein)

361 entries found, searching for "channel"

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4) Extracellular matrix

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[0111] In addition to these, the various keywords shown in the above-mentioned categorization or others can be used for the OMIM search and the result may suggest the involvement thereof in diseases.

[0112] Further, the use of nucleotide sequences of cDNAs of the present invention enables analyzing the expression frequency of genes corresponding to the cDNAs. In addition, functions of the genes can be predicted based on the information obtained by the expression frequency analysis.

[0113] There are several methods for analyzing the expression levels of genes involved in diseases. Differences in gene expression levels between diseased and normal tissues are studied by the analytical methods using, for example, Northern hybridization, RT-PCR, DNA microarray, etc. (Experimental Medicine, Vol.17, No. 8, 980-1056 (1999); Cell Engineering (additional volume) DNA Microarray and Advanced PCR Methods, Muramatsu & Nawa (eds.), Shujinsya (2000)). By computer analysis, in addition to these analysis methods, the nucleotide sequences of expressed genes can be compared to analyze the expression frequency. For example, there is a database called "BCDYPAP"; gene clones are extracted at random from cDNA libraries of various tissues and/or cells, and the clones homologous to one another are assigned to a single cluster based on the information of nucleotide sequence homology at the 3'-end; genes are classified into any clusters, and the numbers of clones in the respective clusters are compared to gain the information on expression frequency (<http://bodymap.lms.u-tokyo.ac.jp/>).

[0114] When explicit difference in the expression levels between diseased tissues and normal tissues is observed for a gene by these analytical methods, it can be concluded that the gene is closely involved in a disease or disorder. Instead of diseased tissues, when gene expression is explicitly different between normal cells and cells reproducing disease-associated specific features, it can be concluded that the gene is closely involved in a disease or disorder.

[0115] From the 1639 clones whose full-length nucleotide sequences had been revealed, genes involved in particular pathology or functions were selected by the use of databases shown below (see Example 7; "Expression frequency analysis *in silico*"). The database used in the analyses of the present invention contains nucleotide sequences of 770,546 clones, and the population of the database is large enough for the analysis. The sequence information in the database was obtained by selecting cDNA clones at random from cDNA libraries derived from the various tissues and cells shown in Example 1 and determining the 5'-end sequences thereof.

[0116] Then, the nucleotide sequences of respective clones in this database were categorized (clustered) based on the nucleotide sequence homology determined with a search program; the number of clones belonging to every cluster of each library was determined and normalized; thus, the ratio of a certain gene in a cDNA library was determined. This analysis provided the information of the expression frequency of a gene in a tissue or cell that is the source of the cDNA library.

[0117] Then, in order to analyze the expression of genes corresponding to the nucleotide sequences of cDNAs of the present invention in tissues and cells, the libraries from the tissues or cells, which had been used in the large-scale cDNA analyses, were taken as subjects to compare the expression levels between different tissues or cells. Namely, the expression frequency was analyzed by comparing the previously normalized values between tissues or cells from which 600 or more cDNA clones whose nucleotide sequences had been analyzed were derived. The result of this analysis showed that the cDNA clones corresponded to the genes involved in the pathology and functions, which are indicated below. Each value in Tables 3 to 39 indicated below represents a relative expression frequency; the higher the value, the higher the expression level.

Osteoporosis-related genes

[0118] Osteoporosis is a pathology in which bones are easily broken owing to overall decrease in components of bone. The onset correlates to the balance between the functions of osteoblast-producing bone and osteoclast-absorbing bone, namely bone metabolism. Thus, the genes involved in the increase of osteoclasts differentiating from precursor cells of monocyte/macrophage line (Molecular Medicine 38, 642-648, (2001)) are genes involved in osteoporosis relevant to bone metabolism.

[0119] A nucleotide sequence information-based analysis was carried out to identify the genes whose expression frequencies are higher or lower in CD34+ cell (cell expressing a glycoprotein CD34) treated with the osteoclast differentiation factor (Molecular Medicine 38, 642-648, (2001)) than in the untreated CD34+ cell, which is the precursor cell of monocyte/macrophage line. The result of comparative analysis for the frequency between the cDNA libraries prepared from the RNA of CD34+ cells (CD34C) and from the RNA of CD34+ cells treated with the osteoclast differentiation factor (D30ST, D60ST or D90ST) showed that the genes whose expression levels were different between the two were 41 clones indicated in Table 3. These clones are involved in osteoporosis.

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Genes involved in neural cell differentiation

[0120] Genes involved in neural cell differentiation are useful for treating neurological diseases. Genes with varying expression levels in response to induction of cellular differentiation in neural cells are thought to be involved in neurological diseases.

[0121] A survey was performed for genes whose expression levels are varied in response to induction of differentiation (stimulation by retinoic acid (RA) or growth inhibitor treatment after RA stimulation) in cultured cells of a neural strain, NT2. The result of comparative analysis of cDNA libraries derived from undifferentiated NT2 cells (NT2RM) and the cells subjected to the differentiation treatment (NT2RP, NT2RI or NT2NE) showed that the genes whose expression levels were different between the two were 500 clones indicated in Table 4. These genes are neurological disease-related genes.

Cancer-related genes

[0122] It has been assumed that, distinct from normal tissues, cancer tissues express a distinct set of genes, and thus the expression thereof can contribute to the carcinogenesis in tissues and cells. Thus, genes whose expression patterns in cancer tissues are different from those in normal tissues are cancer-related genes. Search was carried out for the genes whose expression levels in cancer tissues were different from those in normal tissues.

[0123] The result of comparative analysis of cDNA libraries derived from breast tumor (TBAS) and normal breast (BEAST) showed that the genes whose expression levels were different between the two were 11 clones indicated in Table 5.

[0124] The result of comparative analysis of cDNA libraries derived cervical tumor (TCERX) and normal cervical duct (CERVX) showed that the genes whose expression levels were different between the two were 10 clones indicated in Table 6.

[0125] The result of comparative analysis of cDNA libraries derived from colon tumor (TCOLN) and normal colon (COLON) showed that the genes whose expression levels were different between the two were 5 clones indicated in Table 7.

[0126] The result of comparative analysis of cDNA libraries derived from esophageal tumor (TESOP) and normal esophagus (NESOP) showed that the genes whose expression levels were different between the two were 5 clones indicated in Table 8.

[0127] The result of comparative analysis of cDNA libraries derived from kidney tumor (TKIDN) and normal kidney (KIDNE) showed that the genes whose expression levels were different between the two were 205 clones indicated in Table 9.

[0128] The result of comparative analysis of cDNA libraries derived from liver tumor (TLIVE) and normal liver (LIVER) showed that the genes whose expression levels were different between the two were 35 clones indicated in Table 10.

[0129] The result of comparative analysis of cDNA libraries derived from lung tumor (TLUNG) and normal lung (HLUNG) showed that the genes whose expression levels were different between the two were 62 clones indicated in Table 11.

[0130] The result of comparative analysis of cDNA libraries derived from ovary tumor (TOVER) and normal ovary (NOVER) showed the genes whose expression levels were different between the two were 7 clones indicated in Table 12.

[0131] The result of comparative analysis of cDNA libraries derived from stomach tumor (TSTOM) and normal stomach (STOMA) showed that the genes whose expression levels were different between the two were 41 clones indicated in Table 13.

[0132] The result of comparative analysis of cDNA libraries derived from uterine tumor (TUTER) and normal uterus (UTERU) showed that the genes whose expression levels were different between the two were 94 clones indicated in Table 14.

[0133] The result of comparative analysis of cDNA libraries derived from tongue cancer (CTONG) and normal tongue (NTONG) showed that the genes whose expression levels were different between the two were 178 clones indicated in Table 15.

[0134] These genes are involved in cancers.

[0135] Further, there is a method to search for genes involved in development and differentiation, which is the expression frequency analysis in which the expression levels of genes are compared between developing and/or differentiating tissues and/or cells and adult tissues and/or cells. The genes involved in tissue development and/or differentiation are genes participating in tissue construction and expression of function, and thus are useful genes, which are available for regenerative medicine aiming at convenient regeneration of injured tissues.

[0136] By using the information of gene expression frequency gained from the database of 5'-end nucleotide sequences described above, genes involved in development or differentiation of particular tissues were selected from

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the 1639 clones whose full-length nucleotide sequence had been revealed (see Example 7).

[0137] The result of comparative analysis of cDNA libraries derived from fetal brain (FCBBF, FEBRA or OCBBF) and adult brain (BRACE, BRALZ, BRAMY, BRAWH, BRCAN, BRCCO, BRHIP, BRSSN, BRSTN or BRTHA) showed that the genes whose expression levels were different between the two were 745 clones indicated in Tables 16 to 36.

[0138] The result of comparative analysis of cDNA libraries derived from fetal heart (FEHRT) and adult heart (HEART) showed that the genes whose expression levels were different between the two were 54 clones indicated in Table 37.

[0139] The result of comparative analysis of cDNA libraries derived from fetal kidney (FEKID) and adult kidney (KDNE) showed that the genes whose expression levels were different between the two were 145 clones indicated in Table 38.

[0140] The result of comparative analysis of cDNA libraries derived from fetal lung (FELNG) and adult lung (HLUNG) showed that the genes whose expression levels were different between the two were 745 clones indicated in Table 39. These genes are involved in regeneration of tissues and/or cells.

[0141] The expression frequency or the like can be analyzed by PCR based on the nucleotide sequences of cDNAs of the present invention. There are some known methods for comparing the quantities of amplification products obtained by PCR. For example, the band intensities can be determined by ethidium bromide staining. With RI-labeled or fluorescently labeled primers, the RI signal or fluorescence intensity can be assayed for the quantity of labeled amplification products. Alternatively, the quantity of amplification products can also be determined by measuring the RI signal or the fluorescence intensity from the RI-labeled or fluorescently labeled probe hybridizing to the products. The assay results thus obtained are compared and then the clones exhibiting differences in the expression levels can be selected.

[0142] There are some quantitative PCR methods: a PCR method using internal standards; a competitive PCR, in which the quantification is achieved by adding, to a sample, a dilution series of a known quantity of a template RNA and by comparing the quantity of an amplification product derived from the RNA of interest with the quantity of an amplification product derived from the template RNA. These methods overcome the problems of errors in the amount of amplification products among tubes and of the plateau effect. ATAC-PCR (Adaptor-tagged competitive PCR) is a method of competitive PCR which is practiced by using multiple adaptors of different sizes attached to a gene whose 3'-end nucleotide sequence has previously been determined. The ratio of expression frequency of a single mRNA species from a number of tissues (cells) can be assayed in a single step (Nucleic Acids Research 1997, 25(22): 4694-4696; "DNA Micro-array and Advanced PCR Techniques", Cell Technology, supplement, Eds., Muramatsu and Nawa (Shujunsha, 2000): 104-112).

[0143] If it is observed, by using these analytical methods, that the expression levels of genes are evidently varied during major cellular events (such as differentiation and apoptosis), the genes are involved in the cellular events and accordingly are candidates for disease- and/or disorder-related genes. Further, genes exhibiting tissue-specific expression are genes playing important parts in the tissue functions and, therefore, can be candidates for genes involved in diseases and/or disorders affecting the tissues.

[0144] For example, inflammation is an important biological response that is known to be involved in various diseases. The representative inflammation-inducing factors include TNF- α (Tumor Necrosis Factor- α), LPS (Lipopolysaccharides), etc. Many genes have been identified as genes located downstream of the TNF- α or LPS stimulation. The respective stimulations are transduced through independent pathways of signaling cascade. There exists another signaling cascade for both stimulations, wherein NF- κ B is a common transducing molecule shared by the two stimulations (Cell 1995, 80:529-532). It has also been revealed that many inflammation-related genes, including IL-2, IL-6 and G-CSF, are varied in the expression levels thereof in response to the signal through the common pathway (Trends Genet. 1999, 15(6): 229-235). It is assumed that genes whose expression levels are varied in response to the stimulation of TNF- α or LPS also participate in inflammation.

[0145] Further, the infection of *Helicobacter pylori* to the gastric epithelia is known to cause gastritis and gastroduodenal ulcer (Mebio 2000, July, 17(7): 16-33). Thus, the genes whose expression levels are altered depending on co-culturing cells with *Helicobacter pylori* may be involved in gastritis and gastroduodenal ulcer. A recent study has suggested that *Helicobacter pylori* strongly activates the NF- κ B pathway, via the TRAF2/6-I κ B β pathway, namely, via the same pathway shared by TNF- α (Gastroenterology 2000, 119: 97-108).

[0146] THP-1 cell, which is a human monocyte cell line, was cultured in the presence of TNF- α (Tumor Necrosis Factor- α) or LPS (Lipopolysaccharides). The genes whose expression levels were altered owing to the presence of the agent were searched for, and the result showed that the clones whose expression levels were increased owing to the presence of TNF- α were ADRL10000180, BRACE20030780, BRACE20077640, BRACE20083850, BRAWH20004430, FCBBF10006180, FEBRA20003780, FEBRA20006800, FEBRA20012940, FEBRA20015840, HEART20004480, HLUNG10000370, HLUNG20001160, HSYRA20013320, IMR3220008380, KDNE10001520, KDNE20040540, KDNE20061490, KDNE20062990, NT2NE10001630, NT2NE20003920, NT2NE20005500, NT2RI20014500, NT2RI20016570, NT2RI20078270, NT2RI20083630, NTONG10002570, PAUEN10003220, SKNMCI10000290, STOMA20002570, TESTI20011340, UTERU20004850.

[0147] On the other hand, the clones whose expression levels were decreased owing to the presence of TNF- α were

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BRACE20013400, BRACE20091880, HEART20005060, HLUNG20001760, IMR3220008590, NT2NE10001850, NT2RI20011860, NT2RI20053350, NT2RI20070480, PLACE60047380, STOMA20002890, SYN0V20001770, TRACH20001960.

[0148] Further, the clones whose expression levels were increased owing to the presence of LPS were FCBBF10006180, FEBRA20015840, HLUNG10000370, HLUNG20001160, HSYRA20013320, KIDNE20040540, KIDNE20061490, NT2NE10001630, NT2NE20003920, NT2NE20005500, NT2RI20014500, NT2RI20016570, NT2RI20078270, NTONG10002570, PUAE10003220, STOMA20002570, TESTI20011340. On the other hand, the clones whose expression levels were decreased owing to the presence of LPS were BRACE20013400, BRACE20091880, HEART20005060, HLUNG20001760, NT2RI20070480, UMVEN20001330.

[0149] These clones are involved in inflammation.

[0150] MKN45, which is a gastric cancer cell line, was co-cultured with *Helicobacter pylori*. The genes whose expression levels were altered owing to the presence of *Helicobacter pylori* were searched for, and the result showed that the clones whose expression levels were increased owing to the presence of *Helicobacter pylori* were BRACE10001590, BRACE20079530, BRAWH10001620, FEBRA20006800, KIDNE20003490, KIDNE20040540, KIDNE20050420, NT2NE10001850, STOMA20002890, SYN0V20001770, TESTI10000550, UTERU20004850. On the other hand, the clones whose expression levels were decreased owing to the presence of *Helicobacter pylori* were BRACE20034490, BRACE20077640, BRACE20083850, KIDNE20005170, LIVER20000330, NT2RP60000390, NTONG10000980, UMVEN20001330.

[0151] These clones are involved in gastritis or gastroduodenal ulcer.

[0152] For example, if the polypeptide encoded by the cDNA of the present invention is a regulatory factor of cellular conditions such as growth and differentiation, it can be used for developing medicines as follows. The polypeptide or antibody provided by the invention is injected into a certain kind of cells by microinjection. Then, using the cells, it is possible to screen low molecular weight compounds, etc. by measuring the change in the cellular conditions, or the activation or inhibition of a particular gene. The screening can be performed as follows.

[0153] First, the polypeptide is expressed and purified as recombinant. The purified polypeptide is microinjected into cells such as various cell lines, or primary culture cells, and the cellular change such as growth and differentiation can be examined. Alternatively, the induction of genes whose expression is known to be involved in a particular change of cellular conditions may be detected by the amount of mRNA or polypeptide. Alternatively, the amount of intracellular molecules (low molecular weight compounds, etc.) that is changed by the function of the gene product (polypeptide) which is known to be involved in a particular change of cellular conditions may be detected. The compounds to be screened (both low and high molecular compounds are acceptable) can be added to the culture media and assessed for their activity by measuring the change of the cellular conditions.

[0154] Instead of microinjection, cell lines introduced with the gene obtained in the invention can be used for the screening. If the gene product is turn out to be involved in a particular change in the cellular conditions, the change of the product can be used as a measurement for screening. Once a compound is screened out which can activate or inhibit the function of the polypeptide of the invention, it can be applied for developing medicines.

[0155] If the polypeptide encoded by the cDNA of the present invention is a secretory protein, membrane protein, or protein involved in signal transduction, glycoprotein, transcription, or diseases, it can be used in functional assays for developing medicines.

[0156] In case of a membrane protein, it is most likely to be a polypeptide that functions as a receptor or ligand on the cell surface. Therefore, it is possible to reveal a new relationship between a ligand and receptor by screening the membrane protein of the invention based on the binding activity with the known ligand or receptor. Screening can be performed according to the known methods.

[0157] For example, a ligand against the polypeptide of the invention can be screened in the following manner. Namely, a ligand that binds to a specific polypeptide can be screened by a method comprising the steps of: (a) contacting a test sample with the polypeptide of the invention or a partial peptide thereof, or cells expressing these, and (b) selecting a test sample that binds to said polypeptide, said partial peptide, or said cells.

[0158] On the other hand, for example, screening using cells expressing the polypeptide of the present invention that is a receptor protein can also be performed as follows. It is possible to screen receptors that is capable of binding to a specific polypeptide by using procedures (a) attaching the sample cells to the polypeptide of the invention or its partial peptide, and (b) selecting cells that can bind to the said polypeptide or its partial peptide.

[0159] In a following screening as an example, first the polypeptide of the invention is expressed, and the recombinant polypeptide is purified. Next, the purified polypeptide is labeled, binding assay is performed using a various cell lines or primary cultured cells, and cells that are expressing a receptor are selected (Growth and differentiation factors and their receptors, Shin-Seikagaku Jikken Kouza Vol.7 (1991) Honjyo, Arai, Taniguchi, and Muramatsu edit, p203-236, Tokyo-Kagaku-Doujin). A polypeptide of the invention can be labeled with RI such as ¹²⁵I, and enzyme (alkaline phosphatase etc.).

[0160] Alternatively, a polypeptide of the invention may be used without labeling and then detected by using a labeled

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antibody against the polypeptide. The cells that are selected by the above screening methods, which express a receptor of the polypeptide of the invention, can be used for the further screening of an agonists or antagonists of the said receptor

[0161] Once the ligand binding to the polypeptide of the invention, the receptor of the polypeptide of the invention or the cells expressing the receptor are obtained by screening, it is possible to screen a compound that binds to the ligand and receptor. Also it is possible to screen a compound that can inhibit both bindings (agonists or antagonists of the receptor, for example) by utilizing the binding activities.

[0162] When the polypeptide of the invention is a receptor, the screening method comprises the steps of (a) contacting the polypeptide of the invention or cells expressing the polypeptide of the invention with the ligand, in the presence of a test sample, (b) detecting the binding activity between said polypeptide or cells expressing said polypeptide and the ligand, and (c) selecting a compound that reduces said binding activity when compared to the activity in the absence of the test sample. Furthermore, when the polypeptide of the invention is a ligand, the screening method comprises the steps of (a) contacting the polypeptide of the invention with its receptor or cells expressing the receptor in the presence of samples, (b) detecting the binding activity between the polypeptide and its receptor or the cells expressing the receptor, and (c) selecting a compound that can potentially reduce the binding activity compared to the activity in the absence of the sample.

[0163] Samples to screen include cell extracts, expressed products from a gene library, synthesized low molecular compound, synthesized peptide, and natural compounds, for example, but are not construed to be listed here. A compound that is isolated by the above screening using a binding activity of the polypeptide of the invention can also be used as a sample.

[0164] A compound isolated by the screening may be a candidate to be an agonist or an antagonist of the receptor of the polypeptide. By utilizing an assay that monitors a change in the intracellular signaling such as phosphorylation which results from reduction of the binding between the polypeptide and its receptor, it is possible to identify whether the obtained compound is an agonist or antagonist of the receptor. Also, the compound may be a candidate of a molecule that can inhibit the interaction between the polypeptide and its associated proteins (including a receptor) *in vivo*. Such compounds can be used for developing drugs for precaution or cures of a disease in which the polypeptide is involved.

[0165] Secretory proteins may regulate cellular conditions such as growth and differentiation. It is possible to find out a novel factor that regulates cellular conditions by adding the secretory protein of the invention to a certain kind of cell, and performing a screening by utilizing the cellular changes in growth or differentiation, or activation of a particular gene.

[0166] The screening can be performed, for example, as follows. First, the polypeptide of the invention is expressed and purified in a recombinant form. Then, the purified polypeptide is added to a various kind of cell lines or primary cultured cells, and the change in the cell growth and differentiation is monitored. The induction of a particular gene that is known to be involved in a certain cellular change is detected by the amounts of mRNA and polypeptide. Alternatively, the amount of an intracellular molecule (low-molecular-weight compounds, etc.) that is changed by the function of a gene product (polypeptide) that is known to function in a certain cellular change is used for the detection.

[0167] Once the screening reveals that the polypeptide of the invention can regulate cellular conditions or the functions, it is possible to apply the polypeptide as a pharmaceutical and diagnostic medicine for related diseases by itself or by altering a part of it into an appropriate composition.

[0168] As is above described for membrane proteins, the secretory protein provided by the invention may be used to explore a novel ligand-receptor interaction using a screening based on the binding activity to a known ligand or receptor. A similar method can be used to identify an agonist or antagonist. The resulting compounds obtained by the methods can be a candidate of a compound that can inhibit the interaction between the polypeptide of the invention and an interacting molecule (including a receptor). The compounds may be able to use as a preventive, therapeutic, and diagnostic medicine for the diseases, in which the polypeptide may play a certain role.

[0169] Proteins involved in signal transduction or transcription may be a factor that affects a certain polypeptide or gene in response to intracellular/extracellular stimuli. It is possible to find out a novel factor that can affect a polypeptide or gene by expressing the polypeptide provided by the invention in a certain types of cells, and performing a screening utilizing the activation of a certain intracellular polypeptide or gene.

[0170] The screening may be performed as follows. First, a transformed cell line expressing the polypeptide is obtained. Then, the transformed cell line and the untransformed original cell line are compared for the changes in the expression of a certain gene by detecting the amount of its mRNA or polypeptide. Alternatively, the amount of an intracellular molecule (low molecular weight compounds, etc.) that is changed by the function of a certain gene product (polypeptide) may be used for the detection. Furthermore, the change of the expression of a certain gene can be detected by introducing a fusion gene that comprises a regulatory region of the gene and a marker gene (luciferase, β -galactosidase, etc.) into a cell, expressing the polypeptide provided by the invention into the cell, and estimating the activity of a marker gene product (polypeptide).

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[0171] If the polypeptide or gene of the invention is involved in diseases, it is possible to screen a gene or compound that can regulate its expression and/or activity either directly or indirectly by utilizing the polypeptide of the present invention.

[0172] For example, the polypeptide of the invention is expressed and purified as a recombinant polypeptide. Then, the polypeptide or gene that interacts with the polypeptide of the invention is purified, and screened based on the binding. Alternatively, the screening can be performed by adding with a compound of a candidate of the inhibitor added in advance and monitoring the change of binding activity. In another method, a transcription regulatory region locating in the 5'-upstream of the gene encoding the polypeptide of the invention that is capable of regulating the expression of other genes is obtained, and fused with a marker gene. The fusion is introduced into a cell, and the cell is added with compounds to explore a regulatory factor of the expression of the said gene.

[0173] The compound obtained by the screening can be used for developing pharmaceutical and diagnostic medicines for the diseases in which the polypeptide of the present invention is involved. Similarly, if the regulatory factor obtained in the screening is turn out to be a polypeptide, compounds that can newly affect the expression or activity of the polypeptide may be used as a medicine for the diseases in which the polypeptide of the invention is involved.

[0174] If the polypeptide of the invention has an enzymatic activity, regardless as to whether it is a secretory protein, membrane protein, or proteins involved in signal transduction, glycoprotein, transcription, or diseases, a screening may be performed by adding a compound to the polypeptide of the invention and monitoring the change of the compound. The enzymatic activity may also be utilized to screen a compound that can inhibit the activity of the polypeptide.

[0175] In a screening given as an example, the polypeptide of the invention is expressed and the recombinant polypeptide is purified. Then, compounds are contacted with the purified polypeptide, and the amount of the compound and the reaction products is examined. Alternatively, compounds that are candidates of an inhibitor are pretreated, then a compound (substrate) that can react with the purified polypeptide is added, and the amount of the substrate and the reaction products is examined.

[0176] The compounds obtained in the screening may be used as a medicine for diseases in which the polypeptide of the invention is involved. Also they can be applied for tests that examine whether the polypeptide of the invention functions normally *in vivo*.

[0177] Whether the secretory protein, membrane protein, signal transduction-related protein, glycoprotein-related protein, or transcription-related protein of the present invention is a novel protein involved in diseases or not is determined in another method than described above, by obtaining a specific antibody against the polypeptide of the invention, and examining the relationship between the expression or activity of the polypeptide and a certain disease. In an alternative way, it may be analyzed referred to the methods in "Molecular Diagnosis of Genetic Diseases" (Elles R. edit, (1996) in the series of "Method in Molecular Biology" (Humana Press).

[0178] Proteins involved in diseases are targets of screening as mentioned, and thus are very useful in developing drugs which regulate their expression and activity. Also, the proteins are useful in the medicinal industry as a diagnostic marker of the related disease or a target of gene therapy.

[0179] Compounds isolated as mentioned above can be administered patients as it is, or after formulated into a pharmaceutical composition according to the known methods. For example, a pharmaceutically acceptable carrier or vehicle, specifically sterilized water, saline, plant oil, emulsifier, or suspending agent can be mixed with the compounds appropriately. The pharmaceutical compositions can be administered to patients by a method known to those skilled in the art, such as intraarterial, intravenous, or subcutaneous injections. The dosage may vary depending on the weight or age of a patient, or the method of administration, but those skilled in the art can choose an appropriate dosage properly. If the compound is encoded by polynucleotide, the polynucleotide can be cloned into a vector for gene therapy and used for gene therapy. The dosage of the polynucleotide and the method of its administration may vary depending on the weight or age of a patient, or the symptoms, but those skilled in the art can choose properly.

[0180] The present invention further relates to databases comprising at least a sequence of polynucleotide and/or polypeptide, or a medium recorded in such databases, selected from the sequence data of the nucleotide and/or the amino acids indicated in Table 1. The term "databases" means a set of accumulated information as machine-searchable and readable information of nucleotide sequence. The databases of the present invention comprise at least one of the novel nucleotide sequences of polynucleotides provided by the present invention. The databases of the present invention can consist of only the sequence data of the novel polynucleotides provided by the present invention or can comprise other information on nucleotide sequences of known full-length cDNAs or ESTs. The databases of the present invention can be comprised of not only the information on the nucleotide sequences but also the information on the gene functions revealed by the present invention. Additional information such as names of DNA clones carrying the full-length cDNAs can be recorded or linked together with the sequence data in the databases.

[0181] The database of the present invention is useful for gaining complete gene sequence information from partial sequence information of a gene of interest. The database of the present invention comprises nucleotide sequence information of full-length cDNAs. Consequently, by comparing the information in this database with the nucleotide sequence of a partial gene fragment yielded by differential display method or subtraction method, the information on

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the full-length nucleotide sequence of interest can be gained from the sequence of the partial fragment as a starting clue.

[0182] The sequence information of the full-length cDNAs constituting the database of the present invention contains not only the information on the complete sequences but also extra information on expression frequency of the genes as well as homology of the genes to known genes and known polypeptides. Thus the extra information facilitates rapid functional analyses of partial gene fragments. Further, the information on human genes is accumulated in the database of the present invention, and therefore, the database is useful for isolating a human homologue of a gene originating from other species. The human homologue can be isolated based on the nucleotide sequence of the gene from the original species.

[0183] At present, information on a wide variety of gene fragments can be obtained by differential display method and subtraction method. In general, these gene fragments are utilized as tools for isolating the full-length sequences thereof. When the gene fragment corresponds to an already-known gene, the full-length sequence is easily obtained by comparing the partial sequence with the information in known databases. However, when there exists no information corresponding to the partial sequence of interest in the known databases, cDNA cloning should be carried out for the full-length cDNA. It is often difficult to obtain the full-length nucleotide sequence using the partial sequence information as an initial clue. If the full-length of the gene is not available, the amino acid sequence of the polypeptide encoded by the gene remains unidentified. Thus the database of the present invention can contribute to the identification of full-length cDNAs corresponding to gene fragments, which cannot be revealed by using databases of known genes.

[0184] The present invention has provided 1639 polynucleotides. As has not yet proceeded the isolation of full-length cDNA within the human, the invention has great significance. It is known that secretory proteins, membrane proteins, signal transduction-related proteins, glycoprotein-related proteins, transcription-related proteins, and so on are involved in many diseases. The genes and proteins involved in diseases are useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as a target of gene therapy.

[0185] In particular, cDNA assumed to encode secretory proteins, which were provided by this invention, are very important for the industry since the encoded proteins themselves are expected to be useful as pharmaceutical agents and many disease-related genes may be included in them. In addition, membrane proteins, signal transduction-related proteins, transcription-related proteins, disease-related proteins, and genes encoding them can be used as indicators for diseases, etc. These cDNA are also very important for the industry, which are expected to regulate the activity or expression of the encoded protein to treat diseases, etc.

[0186] Any patents, patent applications, and publications cited herein are incorporated by reference.

[0187] The invention is illustrated more specifically with reference to the following examples, but is not to be construed as being limited thereto.

EXAMPLE 1

Preparation of cDNA library by oligo-capping

(1) Extraction and purchase of mRNA

[0188] Total RNAs as mRNA sources were extracted from human tissues (shown below) by the method as described in the reference (J. Sambrook, E. F. Fritsch & T. Maniatis, Molecular Cloning Second edition, Cold Spring harbor Laboratory Press, 1989). Further, by the method as described in the reference (J. Sambrook, E. F. Fritsch & T. Maniatis, Molecular Cloning Second edition, Cold Spring harbor Laboratory Press, 1989), total RNAs as mRNA sources were extracted from human culture cells and human primary culture cells (shown below) which had been cultivated by the methods described in the catalogs.

[0189] The library names and the origins are indicated below in the order of "Library name: Origin". When a library was prepared by the subtraction method, the item is followed by a description of how to prepare the subtracted library

<Extraction of mRNA from human tissues>

NTONG: Normal tongue;
GTONG: Tongue cancer;
FCBBF: Fetal brain;
OCBBF: Fetal brain;
PLACE: Placenta;
SYNOV: Synovial membrane tissue (from rheumatoid arthritis).

<Extraction of mRNA from culture cells>

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BNGH4: H4 cells (ATCC #HTB-148) ;
 IMR32: IMR32 cells (ATCC #CCL-127) ;
 SKNMC: SK-N-MC cells (ATCC #HTB-10) ;
 3NB69: NB69 cells (RCB #RCB0480) ;
 BGG11: G11 cells (RCB #RCB0763) ;
 NB9N4: NB9 cells (RCB #RCB0477) ;
 SKNSH: SK-N-SH cells (RCB #RCB0426) ;
 NT2RM: NT2 cells (STARATAGENE #204101) ;
 NT2RP: NT2 cells treated with retinoic acid (RA) for 5 weeks to induce the differentiation ;
 NT2RI: NT2 cells treated with RA for 5 weeks to induce the differentiation, followed by the treatment with the growth inhibitor for 2 weeks ;
 NT2NE: NT2 cells were treated with RA and the growth inhibitor for the neuronal differentiation, and the resultant neurons were concentrated and harvested (NT2 Neuron) ;
 NTISM: NT2 cells (STARATAGENE #204101) were treated with RA for 5 weeks to induce the differentiation, and then treated with the growth inhibitor for 2 weeks; mRNA was prepared from the cells and a cDNA library was constructed from the mRNA; the cDNAs of the library whose nucleotide sequences were shared by those of mRNAs from undifferentiated NT2 cells were subtracted by using a Subtract Kit (Invitrogen #K4320-01); the subtracted library (NT2RI-NT2RM) was provided by this procedure.

RCB Indicates that the cell was provided by the Cell Bank, RIKEN GENE BANK, The Institute of Physical and Chemical Research; ATCC indicates that the cell was provided by American Type Culture Collection.
 <Extraction of mRNA from primary culture cells>

ASTRO: Normal human astrocyte NHA5732, Takara Shuzo #CC2565;
 DFNES: Normal human dermal fibroblast (neonatal skin); NHDF-Neo NHDF2564, Takara Shuzo #CC2509;
 MESAN: Normal human mesangial cell NHMC56046-2, Takara Shuzo #CC2559;
 NHNPC: Normal human neural progenitor cell NHNP5958, Takara Shuzo #CC2599;
 PEBLM: Normal human peripheral blood mononuclear cell HPBMC5939, Takara Shuzo #CC2702;
 HSYRA: Human synovocyte HS-RA (from rheumatoid arthritis), Toyobo #T404K-05;
 PUAEN: Normal human pulmonary artery endothelial cells, Toyobo #T302K-05;
 UMVEN: Normal human umbilical vein endothelial cell HUVEC, Toyobo #T200K-05;
 HCASM: Normal human coronary artery smooth muscle cell HCASMC, Toyobo #T305K-05;
 HCHON: Normal human chondrocyte HC, Toyobo #T402K-05;
 HHDP: Normal human dermal papilla cell HDPC, Toyobo #THPCCK-001;
 CD34C: CD34+ cells (AllCells, LLC #CB14435M) ;
 D3OST: CD34+ cells treated with the osteoclast differentiation factor (ODF) for 3 days to induce the differentiation;
 D6OST: CD34+ cells treated with ODF for 6 days to induce the differentiation;
 D9OST: CD34+ cells treated with ODF for 9 days to induce the differentiation.

[0190] Then, total RNAs extracted from the following human tissues were purchased and used as mRNA sources. The library names and the origins are indicated below in the order of "Library name: Origin". When a library was prepared by the subtraction method, the item is followed by a description of how to prepare the subtracted library.

<Purchase of total RNA containing mRNA extracted from human tissues>

ADRGL: Adrenal gland, CLONTECH #64016-1;
 BRACE: Brain (cerebellum), CLONTECH #64035-1;
 BRAWH: Whole brain, CLONTECH #64020-1;
 FEBRA: Fetal brain, CLONTECH #64019-1;
 FELIV: Fetal liver, CLONTECH #64018-1;
 HEART: Heart, CLONTECH #64025-1;
 HLUNG: Lung, CLONTECH #64023-1;
 KIDNE: Kidney, CLONTECH #64030-1;
 LIVER: Liver, CLONTECH #64022-1;
 MAMGL: Mammary Gland, CLONTECH #64037-1;
 PANCR: Pancreas, CLONTECH #64031-1;
 PROST: Prostate, CLONTECH #64038-1;

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SALGL: Salivary Gland, CLONTECH #64026-1;
 SKMUS: Skeletal Muscle, CLONTECH #64033-1;
 SMINT: Small Intestine, CLONTECH #64039-1;
 SPLEN: Spleen, CLONTECH #64034-1;
 STOMA: Stomach, CLONTECH #64090-1;
 TBAES: Breast (Tumor), CLONTECH #64015-1;
 TCERX: Cervix (Tumor), CLONTECH #64010-1;
 TCOLN: Colon (Tumor), CLONTECH #64014-1;
 TESTI: Testis, CLONTECH #64027-1;
 THYMU: Thymus, CLONTECH #64028-1;
 TLUNG: Lung (Tumor), CLONTECH #64013-1;
 TOVAR: Ovary (Tumor), CLONTECH #64011-1;
 TRACH: Trachea, CLONTECH #64091-1;
 TUTER: Uterus (Tumor), CLONTECH #64008-1;
 UTERU: Uterus, CLONTECH #64029-1;
 ADIPS: Adipose, Invitrogen #D6005-01;
 BLADE: Bladder, Invitrogen #D6020-01;
 BRALZ: Cerebral cortex from an Alzheimer patient (Brain, cortex, Alzheimer), Invitrogen #D6830-01;
 CERVX: Cervix, Invitrogen #D6047-01;
 COLON: Colon, Invitrogen #D6050-01;
 NESOP: Esophagus, Invitrogen #D6060-01;
 PERIC: Pericardium, Invitrogen #D6105-01;
 RECTM: Rectum, Invitrogen #D6110-01;
 TESOP: Esophageal (Tumor), Invitrogen #D6860-01;
 TKIDN: Kidney (Tumor), Invitrogen #D6870-01;
 TLIVE: Liver (Tumor), Invitrogen #D6880-01;
 TSTOM: Stomach (Tumor), Invitrogen #D6920-01;
 BEAST: Adult breast, STARATAGENE #735044;
 FEHRT: Fetal heart, STARATAGENE #738012;
 FEKID: Fetal kidney, STARATAGENE #738014;
 FELNG: Fetal lung, STARATAGENE #738020;
 NOVAR: Adult ovary, STARATAGENE #735260;
 BRASW: subtracted library (BRALZ-BRAWH).

[0191] A cDNA library was constructed from mRNA prepared from tissues of cerebral cortex obtained from an Alzheimer patient [BRALZ: Cerebral cortex from an Alzheimer patient (Brain, cortex, Alzheimer), Invitrogen #D6830-01]; the cDNAs of this library whose nucleotide sequences were shared by those of mRNAs from whole brain tissue [BRAWH: Whole brain, CLONTECH #64020-1] were subtracted by using a Subtract Kit (Invitrogen #K4320-01).

[0192] Further, mRNAs extracted and purified as poly A(+) RNAs from the human tissues shown below were purchased. A cDNA library was prepared from an RNA mixture in which the poly A(+) RNA from each tissue had been combined with poly A(-) RNA. The poly A(-) RNA was prepared by removing poly A(+) RNA from the total RNA of whole brain tissue (CLONTECH #64020-1) by using oligo dT cellulose. The library names and the origins are indicated below in the order of "Library name: Origin".

<Purchase of mRNAs of human tissues as poly A(+) RNAs>

BRAMY: Brain (amygdala), CLONTECH #6574-1;
 BRCAN: Brain (caudate nucleus), CLONTECH #6575-1;
 BRCOC: Brain (corpus callosum), CLONTECH #6577-1;
 BRHIP: Brain (hippocampus), CLONTECH #6578-1;
 BRSSN: Brain (substantia nigra), CLONTECH #6580-1;
 BRSTN: Brain (subthalamic nucleus), CLONTECH #6581-1;
 BRTHA: Brain (thalamus), CLONTECH #6582-1.

(2) Preparation of cDNA library

[0193] cDNA library was prepared from each RNA by the improved method (WO 01/04286) of oligo capping [M. Maruyama and S. Sugano, Gene, 138: 171-174 (1994)]. A series of procedures, BAP (Bacterial Alkaline Phosphatase)

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treatment, TAP (Tobacco Acid Pyrophosphatase) treatment, RNA ligation, first strand cDNA synthesis and RNA removal, were carried out using the oligo-cap linker (SEQ ID NO: 3279) and oligo dT primer (SEQ ID NO: 3280), as described in WO 01/04286. Then, the single-stranded cDNA was converted to a double-stranded cDNA by PCR (polymerase chain reaction) using 5' (SEQ ID NO: 3281) and 3' (SEQ ID NO: 3282) PCR primers, and then digested with *Sfi*I. Then, a fraction of cDNA fragments, typically 2-kb or longer (3-kb or longer in some cases), was unidirectionally cloned into a *Dra*III-digested pME18SFL3 vector (Figure 1) (GenBank AB009864, Expression vector); the cDNA library was thus prepared.

[0194] The names of cDNA libraries, which were used in the analysis of full-length cDNA sequences, and their origins are shown in Table 2.

Table 2

Library	Type	Origin, etc.
3NB69	Culture cell	NB69 cells (RCB #RCB0480)
ADRL	Tissue	Adrenal gland (CLONTECH #64016-1)
ASTRO	Primary culture cell	Normal Human Astrocyte NHA5732 (Takara Shuzo #CC2565)
BGGI1	Culture cell	G11 cells (RCB #RCB0763)
BNGH4	Culture cell	H4 cells (ATCC #HTB-148)
BRACE	Tissue	Brain, cerebellum (CLONTECH #64035-1)
BRAWH	Tissue	Brain, whole (CLONTECH #64020-1)
CD34C	Primary culture cell	CD34+ cells (AllCells, LLC #CB14435M)
CTONG	Tissue	Tongue, Cancer
D3OST	Primary culture cell	CD34+ cells (ODF induction for 3 days)
DFNES	Primary culture cell	Normal Human Dermal Fibroblasts (Neonatal Skin); NHDF-Neo NHDF2564 (Takara Shuzo #CC2509)
FCBBF	Tissue	Brain, Fetal
FEBRA	Tissue	Brain, Fetal (CLONTECH #64019-1)
HCASM	Primary culture cell	Human coronary artery smooth muscle cells HCASMC (Toyobo #T305K-05)
HEART	Tissue	Heart (CLONTECH #64025-1)
HHDP	Primary culture cell	Human dermal papilla cells HDPC (Toyobo #THPCK-001)
HLUNG	Tissue	Lung (CLONTECH #64023-1)
HSYRA	Primary culture cell	Human synovocytes from rheumatoid arthritis HS-RA (Toyobo #T404K-05)
IMR32	Culture cell	IMR32 cells (ATCC #CCL-127)
KIDNE	Tissue	Kidney (CLONTECH #64030-1)
LIVER	Tissue	Liver (CLONTECH #64022-1)
MAMGL	Tissue	Mammary Gland (CLONTECH #64037-1)
MESAN	Primary culture cell	Normal human mesangial cells NHMC56046-2 (Takara Shuzo #CC2559)
NB9N4	Culture cell	NB9 cells (RCB #RCB0477)
NESOP	Tissue	Esophagus (Invitrogen #D6060-01)
NHNP	Primary culture cell	Normal human neural progenitor cells NHNP5958 (Takara Shuzo #CC2599)
NT2NE	Culture cell	NT2 cells concentrated after differentiation (NT2 Neuron)
NT2RI	Culture cell	NT2 cells treated by growth inhibitor for 2 weeks after RA induction for 5 weeks
NT2RP	Culture cell	NT2 cells treated by RA for 5 weeks
NTONG	Tissue	Tongue

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Table 2 (continued)

Library	Type	Origin, etc.
OCBBF	Tissue	Brain, Fetal
PANCR	Tissue	Pancreas (CLONTECH #64031-1)
PEBLM	Primary culture cell	Human peripheral blood mononuclear cells HPBMC5939 (Takara Shuzo #CC2702)
PLACE	Tissue	Placenta
PROST	Tissue	Prostate (CLONTECH #64038-1)
PUAEN	Primary culture cell	Human pulmonary artery endothelial cells (Toyobo #T302K-05)
SALGL	Tissue	Salivary Gland (CLONTECH #64026-1)
SKMUS	Tissue	Skeletal Muscle (CLONTECH #64033-1)
SKNMC	Culture cell	SK-N-MC cells (ATCC #HTB-10)
SKNSH	Culture cell	SK-N-SH cells (RCB #RCB0426)
SMINT	Tissue	Small Intestine (CLONTECH #64039-1)
SPLEN	Tissue	Spleen (CLONTECH #64034-1)
STOMA	Tissue	Stomach (CLONTECH #64090-1)
SYNOV	Tissue	Synovial membrane tissue from rheumatoid arthritis
TESTI	Tissue	Testis (CLONTECH #64027-1)
THYMU	Tissue	Thymus (CLONTECH #64028-1)
TRACH	Tissue	Trachea (CLONTECH #64091-1)
UMVEN	Primary culture cell	Human umbilical vein endothelial cells HUVEC (Toyobo #T200K-05)
UTERU	Tissue	Uterus (CLONTECH #64021-1)

[0195] The cDNA library with the high fullness ratio (the fullness ratio of 5'-end, which was calculated for each cDNA library by using the protein coding region found in known mRNA species as an index, was 90% in average) prepared by the improved oligo-capping method was constructed by using a eukaryotic expression vector pME18SFL3. The vector contains SR α promoter and SV40 small t Intron in the upstream of the cloning site, and SV40 polyA added signal sequence site in the downstream. As the cloning site of pME18SFL3 has asymmetrical DraIII sites, and the ends of cDNA fragments contain SfiI sites complementary to the DraIII sites, the cloned cDNA fragments can be inserted into the downstream of the SR α promoter unidirectionally. Therefore, clones containing full-length cDNA can be expressed transiently by introducing the obtained plasmid directly into COS cells, etc. Thus, the clones can be analyzed very easily in terms of the proteins that are the gene products of the clones, or in terms of the biological activities of the proteins.

(3) Assessment of the 5'-end completeness of clones derived from the cDNA library prepared by oligo-capping

[0196] With respect to the plasmid DNAs of clones derived from the libraries, the nucleotide sequences of cDNA 5'-ends (3'-ends as well in some cases) were determined in a DNA sequencer (ABI PRISM 3700, PE Biosystems), after sequencing reaction was conducted by using a DNA sequencing reagent (BigDye Terminator Cycle Sequencing FS Ready Reaction Kit, PE Biosystems) according to the manual. A database was constructed based on the obtained data.

[0197] The 5'-end completeness of about 770,000 clones derived from the human cDNA libraries prepared by the improved oligo-capping method was determined by the following method. The clones whose 5'-end sequences were consistent with those of known human mRNA in the public database were judged to be "full-length" if they had a longer 5'-end sequence than that of the known human mRNA; or even though the 5'-end sequence was shorter, if it contained the translation initiation codon it was judged to have the "full-length" sequence. Clones which did not contain the translation initiation codon were judged to be "not-full-length". The fullness ratio ((the number of full-length clones)/(the number of full-length and not-full-length clones)) at the 5'-end of the cDNA clones was determined by comparing with known human mRNA. As a result, the fullness ratio of the 5'-ends was 90%. The result indicates that the fullness ratio

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at the 5'-end sequence was extremely high in the human cDNA clones obtained by the oligo-capping method.

EXAMPLE 25 Sequencing analysis of cDNA ends and selection of full-length clones

[0198] With respect to the plasmid DNAs of clones obtained from each cDNA library, the 5'-end nucleotide sequences of the cDNAs were determined in a DNA sequencer (ABI PRISM 3700, PE Biosystems), after sequencing reaction was conducted by using a DNA sequencing reagent (Dye Terminator Cycle Sequencing FS Ready Reaction Kit, dRhod-

amine Terminator Cycle Sequencing FS Ready Reaction Kit or BigDye Terminator Cycle Sequencing FS Ready Reaction Kit, PE Biosystems) according to the manual. A database was constructed using the data obtained.

[0199] For the analyzed 5'-end sequences of cDNA clones, the data with the annotation of "complete cds" in the GenBank and UniGene were searched by BLAST homology search. When identical to certain human mRNA sequences, such cDNA clones were excluded. Then, clustering was carried out. When the identity was 90% or higher, and the length of consensus sequence was 50 base pairs or longer, the cDNA clones were assumed to belong to an identical cluster, and thus clustered. cDNA clones longer in the 5' direction were selected from the members belonging to a cluster; if required, the 3'-end sequences of the selected clones were determined by the same analysis method as used to determine the 5'-end sequences. The data of the end sequences obtained were analyzed, and then the clones forming a sequence contig at 5'- and 3'-ends were excluded. Further, as mentioned above, the data was analyzed again by BLAST homology search; when identical to certain human mRNA sequences (including sequences patented and applied for), the cDNA clones were excluded. Thus, the cDNAs clones to be analyzed for their nucleotide sequence were obtained.

EXAMPLE 325 Analysis of the full-length nucleotide sequences

[0200] The full-length nucleotide sequences of the selected clones were determined. The nucleotide sequence determination was mainly performed by primer walking method comprising the dideoxy terminator method using custom-made synthetic DNA primers. Namely, the nucleotide sequences of the DNAs were determined in a sequencer from PE Biosystems, after sequencing reaction was carried out with a DNA sequencing reagent from the same supplier using the custom-made synthetic DNA primers according to the manual. A part of the clones were analyzed with a DNA sequencer from Licor.

[0201] Further, the nucleotide sequences of a part of the clones were determined by the shotgun method where the plasmids containing the cDNAs were digested at random were used, instead of the use of custom-made primers, by the same method in the DNA sequencer. The full-length nucleotide sequences were finally determined by completely assembling the partial nucleotide sequences obtained by the above method.

[0202] Then, the regions translatable to proteins were deduced from the determined full-length nucleotide sequences, and thereby the amino acid sequences were determined. SEQ ID NOs corresponding to the respective sequences are shown in Table 1.

EXAMPLE 445 Functional prediction by homology search

[0203] For the determined nucleotide sequences, GenBank, SwissProt, UniGene, and nr were searched by BLAST. The clones exhibiting higher homology, which were convenient to predict their functions based on the nucleotide sequences and deduced amino acid sequences, were selected based on the BLAST search hit data whose P value or E value was 10^{-4} or lower and for which the length of consensus sequence \times homology = 30 or higher in the amino acid database search. Further, from them, representative clones were selected, which are shown as Homology Search Result Data in the last part herein. Accordingly, the data shown herein are merely the representative data, and the molecule exhibiting homology to each clone is not limited thereto. Further, with respect to a part of clones, the BLAST search hit data that did not meet the criteria as described above are not shown herein.

EXAMPLE 5

Search for signal sequence, transmembrane domain and other functional domains in the deduced amino acid sequences

[0204] With respect to the amino acid sequences deduced from the full-length nucleotide sequences, the prediction was made for the presence of signal sequence at the amino terminus, the presence of transmembrane domain, and the presence of functional protein domains (motifs). The signal sequence at the amino terminus was searched for by PSORT [K. Nakai & M. Kanehisa, *Genomics*, 14: 897-911 (1992)]; the transmembrane domain, by SOSUI [T. Hirokawa et al., *Bioinformatics*, 14: 378-379 (1998)] (Mitsui Knowledge Industry); the function domain, by Pfam (<http://www.sanger.ac.uk/Software/fam3.html>). The amino acid sequence in which the signal sequence at the amino terminus or transmembrane domain had been predicted to be present by PSORT or SOSUI were assumed to be a secretory or membrane protein. Further, when the amino acid sequence hit a certain functional domain by the Pfam functional domain search, the protein function can be predicted based on the hit data, for example, by referring to the function categories on the PROSITE (<http://www.expasy.ch/cgi-bin/prosite-list.pl>). In addition, the functional domain search can also be carried out on the PROSITE.

[0205] The search results obtained with the respective programs are shown below.

[0206] The clones whose deduced amino acid sequences were detected to have the signal sequences by PSORT are as follows.

ADRLG10001600, BGGI120010970, BNGH410001180, BNGH410001370, BRACE10001690, BRACE20010650, BRACE20014920, BRACE20079530, BRACE20086550, BRACE20089600, BRAWH20004430, BRAWH200040950, BRAWH20052250, BRAWH20092610, CD34C20000510, CTONG20028160, FEBRA20003780, FEBRA20004150, FEBRA20006900, FEBRA20008090, FEBRA20012270, FEBRA20015840, FEBRA20020860, FEBRA20021910, FEBRA20037070, HHDPC20000950, HLUNG10000240, HLUNG20001250, HSYRA20003470, HSYRA20014200, IMR3210001580, IMR3220007750, IMR3220008590, KIDNE10001430, KIDNE20001670, KIDNE20003300, KIDNE20042620, KIDNE20054000, KIDNE20060530, KIDNE20066520, LIVER10005420, MAMGL10000320, NHNPC20002060, NT2NE10001630, NT2NE20016260, NT2NE20055170, NT2RI20009740, NT2RI20015400, NT2RI20030110, NT2RI20042840, NT2RI20053350, NT2RI20070840, NT2RI20073030, NT2RI20074980, NT2RI20078270, NT2RI20092890, NT2RP70015910, NT2RP70021510, NT2RP70029820, NT2RP70047900, NT2RP70074220, NT2RP70079250, NT2RP70091680, NT2RP70094290, NT2RP70094980, NT2RP70095070, NTONG10000980, NTONG10002140, NTONG10002570, OCBF10000420, PANC100000210, PLACE60020840, PLACE60026990, PLACE60043960, PLACE60049930, PLACE60050290, PROST10005260, PROST10005360, PROST20000360, PROST20029600, PROST20044160, PROST20054260, PROST20058800, SVINT10000160, SPLEN10000910, SPLEN20001340, STOMA20002570, TESTI20026320, TESTI20026980, TESTI20027070, TESTI20028660, TESTI20042870, TESTI20049940, THYMU10000830, UTERU10001920, UTERU20003930, UTERU20004850

[0207] The clones whose deduced amino acid sequences were detected to have the transmembrane domains by SOSUI are as follows. Numerals indicate the numbers of transmembrane domains detected in the deduced amino acid sequences. Of the search result, the clone name and the number of transmembrane domains are demarcated by a double slash mark (/).

3NB6910000180/4, 3NB6910000850/1, 3NB6920000290/2, 3NB6920003300/5, 3NB6920005450/2, ADRLG10000180/1, ADRLG10001600/1, ADRLG20003230/2, BGGI120010970/1, BNGH410000800/2, BNGH41000104/2, BNGH410001370/1, BNGH410001980/1, BRACE20007180/1, BRACE20010650/1, BRACE2001170/2, BRACE20013400/2, BRACE20013520/2, BRACE20014230/2, BRACE20014530/1, BRACE20014920/1, BRACE20018590/1, BRACE20022270/1, BRACE20026850/1, BRACE20030780/3, BRACE200310010/10, BRACE20034490/2, BRACE20071380/3, BRACE20071970/1, BRACE20072810/2, BRACE20075020/1, BRACE20075380/3, BRACE20076410/1, BRACE20076850/1, BRACE20077610/2, BRACE20077640/2, BRACE20077980/1, BRACE20086550/1, BRACE20089600/1, BRACE20091880/1, BRAWH10000010/1, BRAWH10000370/1, BRAWH10000940/1, BRAWH10001620/1, BRAWH10001800/1, BRAWH20004430/8, BRAWH20006970/1, BRAWH20011290/4, BRAWH20014380/2, BRAWH20015030/2, BRAWH20036930/1, BRAWH20038320/2, BRAWH20059980/1, BRAWH20087060/1, BRAWH20092610/3, CD34C20000510/1, CTONG20015330/1, CTONG20028160/2, CTONG20037820/1, CTONG20047160/4, FCBBF10006180/3, FCBBF10006750/2, FCBBF20005910/1, FCBBF20009400/3, FCBBF20015380/5, FEBRA20004040/2, FEBRA20004150/3, FEBRA20004520/3, FEBRA20004910/2, FEBRA20006860/3, FEBRA20008800/1, FEBRA20010930/7, FEBRA20012450/3, FEBRA20012940/1, FEBRA20013510/2, FEBRA20014870/1, FEBRA20015840/2, FEBRA20020860/2, FEBRA20021910/1, FEBRA20031550/2, FEBRA20041910/1, FEBRA20063150/1, FEBRA2006670/2, HCASM10000610/2, HCASM20002020/1, HEART20000990/1, HEART20004920/2, HHDPC20000950/2, HLUNG10000370/2, HLUNG20001160/1,

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HLUNG20001420/1/2, HLUNG20001760/2, HSYRA20003470/1, HSYRA20008280/1, HSYRA20011030/1
 HSYRA20015800/2, IMR321000440/1, IMR3210001580/2, IMR3210002660/6, IMR3220008590/1,
 IMR3220009840/2, KIDNE10001040/1, KIDNE10001430/1, KIDNE20000700/1, KIDNE20000850/1,
 KIDNE20001670/7, KIDNE20003150/1, KIDNE20003300/7, KIDNE20003490/4, KIDNE20004220/1, KIDNE20004410/3
 5 KIDNE20005170/2, KIDNE20003050/2, KIDNE20003570/1, KIDNE20003910/5, KIDNE20004410/3
 KIDNE200448280/12, KIDNE20049810/2, KIDNE20054770/12, KIDNE20060530/2, KIDNE20060620/2,
 KIDNE20063530/1, KIDNE20068520/2, KIDNE20067800/1, KIDNE20071860/1, KIDNE20074220/1,
 KIDNE20075690/5, LIVER10000580/3, LIVER10000670/1, LIVER10001040/2, LIVER10001110/1,
 LIVER10001750/1, LIVER20004180/1, MAMGL10001780/1, MAMGL10001840/2, MESAN10001470/1,
 10 MESAN10001800/7, MESAN20001490/2, NB9N42000420/1, NHNPC20002060/2, NT2NE10000230/1,
 NT2NE10001850/6, NT2NE20003920/1, NT2NE20004550/1, NT2NE20004700/1, NT2NE20005500/1,
 NT2NE20012470/2, NT2NE20014350/1, NT2NE20016260/4, NT2NE20034080/2, NT2NE20047160/1,
 NT2NE20055170/3, NT2NE20057200/1, NT2RI20005970/7, NT2RI20014490/11, NT2RI20016570/2,
 NT2RI20018460/1, NT2RI20018660/2, NT2RI20021520/7, NT2RI20022430/4, NT2RI20022520/3,
 15 NT2RI20030310/1, NT2RI20030510/2, NT2RI20033830/2, NT2RI20036780/1, NT2RI20044420/1,
 NT2RI20044980/2, NT2RI20050870/8, NT2RI20051005/1, NT2RI20068250/11, NT2RI20068250/11,
 NT2RI20070480/1, NT2RI20077540/4, NT2RI20078790/1, NT2RI20081880/3, NT2RI20085980/3,
 NT2RI20092890/2, NT2RI20094060/4, NT2RP60000320/10, NT2RP60000390/1, NT2RP60001090/1,
 20 NT2RP70002380/4, NT2RP70002590/5, NT2RP70003640/1, NT2RP70004770/4, NT2RP70006240/1,
 NT2RP70011660/11, NT2RP700115910/2, NT2RP70021510/1, NT2RP70023790/2, NT2RP70026190/2,
 NT2RP70043730/3, NT2RP70047900/2, NT2RP70049250/1, NT2RP70064080/3, NT2RP70071540/2,
 NT2RP70071770/13, NT2RP70072520/2, NT2RP70073810/3, NT2RP70075040/4, NT2RP70076170/2,
 NT2RP70079750/2, NT2RP70081330/2, NT2RP70081370/8, NT2RP70085500/2, NT2RP70090120/10,
 NT2RP70091490/3, NT2RP70093220/11, NT2RP70093730/1, NT2RP70094290/1, NT2RP70094810/11/2,
 25 NT2RP70094980/3, NTONG10002570/2, NTONG20002850/4, NTONG20004920/1, NTONG20008000/1,
 NTONG20012220/1, OCBF20002310/2, OCBF20009980/1, OCBF20012100/2, PLACE50000670/1,
 PLACE50001050/1, PLACE60005550/2, PLACE60012810/2, PLACE60018860/7, PLACE60020160/1,
 PLACE60020840/6, PLACE60037050/1, PLACE60037450/1, PLACE60047380/1, PLACE60049930/1,
 PLACE60055290/1, PROST10002200/2, PROST10002720/1, PROST10005360/1, PROST20000360/1,
 30 PROST20001760/4, PROST20029600/2, PROST20033020/1, PROST20039220/3, PROST20044160/1,
 PROST20051430/1, PROST20054260/5, PROST20059190/3, PROST20059430/3, PROST20069880/1,
 PROST20072370/1, PUAEN10000570/1, PUAEN10001610/1, PUAEN10003220/1, SKMUS20007740/1,
 SKNMC10000190/1, SKNMC10000290/1, SKNMC10002290/2, SKNMC10002510/8, SMINT10000160/2,
 SMINT10000420/8, SMINT10000570/2, SMINT10001180/1, SMINT20000180/2, SMINT20002770/3,
 35 SPLEN200001340/1, SPLEN20002430/1, SPLEN20002700/1, SPLEN20003100/1, SPLEN20004960/2,
 STOMA10000520/2, STOMA100001170/1, STOMA20000320/1, STOMA20002570/3, SYNVO20001770/2,
 TEST10000420/1, TEST10000960/1, TEST10006000/1, TEST10009090/1, TEST10009700/7,
 TEST12001130/5, TEST120012370/1, TEST120013520/4, TEST120014200/9, TEST120016210/2,
 TEST120016710/1, TEST120018620/2, TEST12002020/2, TEST120020810/8, TEST120022510/3,
 40 TEST120024670/2, TEST12002580/2, TEST120026980/2, TEST120027000/1, TEST120030370/1,
 TEST120031930/1, TEST120042870/3, TEST120047120/5, TEST12004940/2, TEST120057420/1,
 TEST120058600/6, TEST120067740/2, TEST120069780/3, TEST120074800/5, TEST120077490/4,
 TEST120079510/3, TEST120080200/7, TEST120081440/1, TEST120087740/2, TEST120088470/2,
 TEST120136910/1, THYMU10001760/1, THYMU10003290/1, THYMU10003820/4, THYMU10005580/4,
 45 TRACH10000630/3, TRACH100001000/1, TRACH10001400/1, TRACH20001850/2, TRACH200001960/2,
 TRACH20004960/2, TRACH20006650/11, TRACH20007670/2, TRACH20008980/2, TRACH20015920/2,
 UMVEN20001330/2, UTERU10000770/2

[0208] The Names of clones whose deduced amino acid sequences were detected to have functional domains with Pfam, and the name of hit functional domains are as follows. The search result is indicated as "clone name/functional domain name". When the clone has multiple hit functional domains, they are listed and demarcated by a double slash mark (/). When the clone has multiple hits of an identical functional domain, each is listed without abridgment.

3NB6910000180/TS-N domain/UBA domain
 3NB6910001160/START domain
 3NB6910001290/KRAB box

55 3NB6910001730/R/O1/2K632.3/MJ0444 family
 3NB6920002810/DEAD/DEAH box helicase/conserved C-terminal domain 3NB6920009120/Zinc finger,
 C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/1/rataxin-like domain
 3NB6920010020/Regulator of G protein signaling domain

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3NB6920014330//Domain of unknown function
 3NB6920014710//DNA binding domain with preference for A/T rich regions//Zinc finger, C2H2 type
 3NB6920015110//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)//RNA recognition motif. (a.k.a. RRM,
 RBD, or RNP domain)
 5 3NB6920015570//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2
 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2
 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 ADRL1 10000020//BTB/POZ domain//Kelch motif//Kelch motif
 ADRL1 10000650//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc
 10 finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 ADRL1 10001600//Cytochrome P450//Cytochrome P450 ADRL1 10001650//Urease//Chlorohydrolase//Dihydroorota-
 se-like
 ADRL20000740//Dockerin domain type I//RhoGAP domain
 ASTR010000180//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain,
 G-beta repeat
 15 ASTR020000950//SNAP-25 family
 ASTR020004170//Ribonuclease T2 family
 BGGI120005330//MP dehydrogenase / GMP reductase N terminus//CBS domain//CBS domain//Dihydroorotate de-
 hydrogenase//Histidine biosynthesis protein//FMN-dependent dehydrogenase//Conserved region in glutamate syn-
 20 thase//MP dehydrogenase / GMP reductase C terminus
 BGGI120005440//Importin beta binding domain
 BGGI120006840//Sir2 family
 BGGI120006930//Gollagen triple helix repeat (20 copies)//SAM domain (Sterile alpha motif)
 BGGI120010970//F5/8 type C domain//Laminin G domain//Laminin G
 25 domain//Fibrinogen beta and gamma chains, C-terminal globular domain
 BGGI120017140//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2
 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 BNGH41 0000290//SPRY domain
 BNGH41 0000340//Prolyl oligopeptidase family//Phospholipase/Carboxyesterase
 30 BNGH41 0001040//Eukaryotic protein kinase domain
 BNGH41 0001180//Low-density lipoprotein receptor domain class A//Low-density lipoprotein receptor domain class A//
 Low-density lipoprotein receptor domain class A//WAP-type (Whey Acidic Protein) 'four-disulfide core'//Low-density
 lipoprotein receptor domain class A//Low-density lipoprotein receptor domain class A//Low-density lipoprotein receptor
 domain class A//Low-density lipoprotein receptor domain class A//long chain scorpion toxins//Chitin binding Peritrophin-
 35 A domain//Low-density lipoprotein receptor repeat class B//Low-density lipoprotein receptor repeat class B//Low-density
 lipoprotein receptor repeat class B//Low-density lipoprotein receptor repeat class B//Low-density lipoprotein re-
 ceptor repeat class B
 BNGH41 0001370//Filamin/ABP280 repeat.
 BNGH41 0001770//MP dehydrogenase / GMP reductase N terminus//CBS domain//CBS domain//Dihydroorotate de-
 40 hydrogenase//Histidine biosynthesis protein//FMN-dependent dehydrogenase//Conserved region in glutamate syn-
 thase//MP dehydrogenase / GMP reductase C terminus
 BNGH41 0001900//Viral (Superfamily 1) RNA helicase
 BNGH41 0001980//POT family//Bacteriorhodopsin//Sugar (and other) transporter
 BNGH420005320//SCAN domain//KRAB box//Zinc finger, C2H2 type//GATA zinc finger//Zinc finger, C2H2 type//Zinc
 45 finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2
 type
 BRACE1 0000420//Fatty acid desaturase//Protein phosphatase 2C
 BRACE1 0000930//Zinc finger, C3HC4 type (RING finger)/TRAF-type zinc finger//TRAF-type zinc finger//MATH do-
 main
 50 BRACE1 0001150//DNA gyrase/topoisomerase IV, subunit A//Nucleosome assembly protein (NAP)
 BRACE1 0001660//Zinc finger, C2H2 type
 BRACE20002800//IQ calmodulin-binding motif
 BRACE20005650//ATP synthase ab C terminal
 BRACE20006980//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat
 55 BRAGE20007180//Calcitonin / CGRP / IAPP family
 BRACE20008850//Zinc finger, C3HC4 type (RING finger)
 BRACE20010650//F-box domain.
 BRACE20013750//Hepatitis C virus non-structural protein NS4a

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[illegible]

[illegible]

S-11 (TFIIS)/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type
FEBRA20005360//Cystatin domain
FEBRA20007330//EF hand/EF hand
FEBRA20007870//Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/
Zinc finger, C2H2 type
FEBRA20008560//Importin beta binding domain/Armadillo/beta-catenin-like repeats
FEBRA20008810//Actin
FEBRA20097250//KRAB box/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2
type/Zinc finger, C2H2 type/Bol A-like protein/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/
Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type FEBRA20011330//Trypsin and protease inhibitors/
PCI domain
FEBRA20011460//SCAN domain
FEBRA20012450//Leucine rich repeat N-terminal domain/Leucine Rich Repeat/Leucine Rich Repeat/Leucine Rich
Repeat/Leucine Rich Repeat/Leucine Rich Repeat/Leucine Rich Repeat/Leucine Rich Repeat/Leucine rich repeat
C-terminal domain/Immunoglobulin domain/Fibronectin type III domain
FEBRA20014920//S-adenosylmethionine synthetase
FEBRA20015840//EGF-like domain/EGF-like domain/EGF-like domain/EGF-like domain/EB module/EGF-like do-
main/EGF-like domain
FEBRA20017600//Immunoglobulin domain
FEBRA20017150//Zinc finger, C3HC4 type (RING finger)/Zinc finger, C3HC4 type (RING finger)/Insulin-like growth
factor binding proteins/B-box zinc finger//CONSTANS family zinc finger/B-box zinc finger//Putative zinc finger in N-
recoignin/Fibronectin type III domain//SPRY domain
FEBRA20019890//PH domain/Putative GTP-ase activating protein for Arf//Ank repeat//Ank repeat
FEBRA20024290//RNA polymerase alpha subunit
FEBRA20024420//GMC oxidoreductases
FEBRA20025250//TBC domain
FEBRA20034290//CAP-Gly domain
FEBRA20043250//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat/Homoeobox associated leucine zipper
FEBRA20043290//Myosin tail/tactate/malate dehydrogenase/Troponin//Domain present in Hsp70 regulators//Inter-
leukin-6/G-CSF/MGF family//Myosin tail
FEBRA20044900//Pou domain - N-terminal to homoeobox domain//Spectrin repeat//Spectrin repeat
FEBRA20045920//Glycoprotease family
FEBRA20050140//Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc
finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc
finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/
Dual specificity phosphatase, catalytic domain
FEBRA20057260//TBC domain
FEBRA20057880//PDZ domain (Also known as DHR or GLGF).
FEBRA20060920//DIX domain
FEBRA20062700//haloacid dehalogenase-like hydrolase
FEBRA20064760//Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc
finger, C2H2 type/DIM DNA binding domain/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/
Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/
Zinc finger, C2H2 type/PHD-finger/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2
type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2
type
FEBRA20066670//Transferrin precursor (formerly prealbumin)
FEBRA20067360//KRAB box/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2
type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2
type
FEBRA20069420//KRAB box/Zinc finger, C2H2 type/Ribosomal protein L37e/Zinc finger, C2H2 type/Zinc finger,
C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger,
C2H2 type/Zinc finger, C2H2 type
FEBRA20070170//PX domain
FEBRA20072000//TPR Domain//TPR Domain//TPR Domain//TPR Domain//TPR Domain//TPR Domain//TPR Domain//
FEBRA20075510//Ras family
HCASM20002140//Cyclin
HCASM20003070//RNA recognition motif, (a.k.a. RRM, RBD, or RNP domain)

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- HEART20004110//POT family
 HEART20005060//Occludin/ELL family//K-box region
 HEART20005680//Nerve growth factor family
 5 HHDP20000950//Viral (Superfamily 1) RNA helicase//NB-ARC domain//Adenylate kinase//Adenylate kinase
 HHDP20001150//Collagen triple helix repeat (20 copies)//C1q domain
 HHDP20001490//UJA domain//Integrase Zinc binding domain//IBR domain//IBR domain
 HHDP20003150//Zn-finger in Ran binding protein and others//Zinc knuckle
 HHDP20004550//FERM domain (Band 4.1 family)
 10 HHDP20004560//2S seed storage family
 HHDP20004620//FAD binding domain
 HLUNG10000240//Transforming growth factor beta like domain
 HLUNG10000370//TPR Domain//TPR Domain//TPR Domain//TPR Domain
 HLUNG10000760//HMG (high mobility group) box
 15 HLUNG10000990//Adenosylmethionine decarboxylase
 HLUNG20000680//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//PHD-finger//
 Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//
 Zinc finger, C2H2 type
 20 HLUNG20001420//REV protein (anti-repression trans-activator protein)//Bacteriorhodopsin//Photosystem II reaction
 centre T protein//Sugar (and other) transporter//FecCD transport family
 HLUNG20001760//Transferrin precursor (formerly prealbumin)
 HLUNG20002550//Trypsin
 HSYRA10001190//TBC domain
 HSYRA10001370//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//PHD-finger//
 25 Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc
 finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 HSYRA10001680//DEAD/DEAH box helicase
 HSYRA10001780//Alpha-2-macroglobulin family N-terminal region
 HSYRA20001350//F-box domain//Kelch motif//Kelch motif//Kelch motif
 30 HSYRA20005100//JvrD/REP helicase
 HSYRA20013320//Insulin-like growth factor binding proteins//Thyroglobulin type-1 repeat
 HSYRA20014760//Von Willebrand factor type A domain
 HSYRA20015740//Glucosamine-6-phosphate isomerase
 HSYRA20016210//HesB-like domain
 35 HSYRA20016310//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//PHD-finger//Zinc finger,
 C2H2 type//Phorbol esters/diacylglycerol binding domain (C1 domain)//Zinc finger, C2H2 type
 IMR3210000440//ATP1G1/PLM/MAT8 family//Eukaryotic protein kinase domain
 IMR3210001580//Extracellular link domain//Lectin C-type domain
 IMR3210002420//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2
 40 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 IMR3210002660//Calion efflux family
 IMR3220002230//FHA domain//HIT family
 IMR3220003020//Src homology domain 2
 IMR3220007420//Zinc finger, C2H2 type
 45 IMR3220007750//Nerve growth factor family//Kazal-type serine protease inhibitor domain//Thyroglobulin type-1 re-
 peat//EF hand//Immunoglobulin domain//Immunoglobulin domain
 IMR3220008380//Formyl transferase
 IMR3220009190//Influenza Matrix protein (M1)//metallopeptidase family M24
 IMR3220009730//Kinesin motor domain
 50 IMR3220012180//IRNA pseudouridine synthase
 IMR3220013170//Dual specificity phosphatase, catalytic domain
 KIDNE10001040//Myb-like DNA-binding domain//Apolipoprotein A1/A4/E family//Thymidylate kinase//SNAP-25 fami-
 ly//Syntaxin
 KIDNE20000410//Aminotransferases class-III pyridoxal-phosphate
 55 KIDNE20000810//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc
 finger, C2H2 type//Zinc finger, C2H2 type//AN1-like Zinc finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//PHD-
 finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 KIDNE20001670//Sugar (and other) transporter

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KIDNE20003150//Major intrinsic protein
 KIDNE20003300//DnaJ domain
 KIDNE20003490//Ubiquitin family//Viral matrix protein//Src homology domain 2//Acylation transferase
 KIDNE20003750//G2 domain
 5 KIDNE20004030//RNA helicase
 KIDNE20004970//Kinesin motor domain//K-box region
 KIDNE20005130//Aminotransferases class-III pyridoxal-phosphate//Aminotransferases class-III pyridoxal-phosphate
 KIDNE20005170//Uncharacterized membrane protein family UPF0013
 KIDNE20031850//Ras association (RalGDS/AF-6) domain
 10 KIDNE20033050//Amidase//Amidase
 KIDNE20033730//SH3 domain//RhoGEF domain//PH domain
 KIDNE20039940//DNA gyrase/topoisomerase IV, subunit A//SCAN domain//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 KIDNE20040840//Eukaryotic protein kinase domain//Phosphoribulokinase//Myosin head (motor domain)//Myosin head
 15 (motor domain)
 KIDNE20043440//Ribosomal protein L36
 KIDNE20044110//Viral methyltransferase//V-type ATPase 116kDa subunit family
 KIDNE20046810//Diene/acetone hydrolase family
 KIDNE20048280//Amino acid permease//Sodium:neurotransmitter symporter family KIDNE20050420//Herpesvirus
 20 UL25 family//Beige/BEACH domain//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//AN1-like Zinc finger//FYVE zinc finger
 KIDNE20052960//Actin
 KIDNE20054770//Transmembrane amino acid transporter protein//Ion transport protein//Amino acid permease
 KIDNE20056290//Acetyltransferase (GNAT) family
 25 KIDNE20056760//Gelsolin homology (CH) domain
 KIDNE20059080//Armadillo/beta-catenin-like repeats//Armadillo/beta-catenin-like repeats//Armadillo/beta-catenin-like repeats
 KIDNE20060140//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
 30 KIDNE20060300//MuT-like domain
 KIDNE20060530//Glycosyl transferase family 8
 KIDNE20061490//SPRY domain
 KIDNE20062480//Scorpion short toxins
 KIDNE20062990//PH domain
 35 KIDNE20066520//Bacterial extracellular solute-binding proteins, family 5
 KIDNE20067600//Immunoglobulin domain//Immunoglobulin domain
 KIDNE20073520//WW domain
 KIDNE20075890//PMP-22/EMP/MP20/Claudin family
 KIDNE20078100//Ribosomal protein L15//Integrase core domain//dUTPase
 40 KIDNE20078110//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//PHD-finger//Zinc finger, C2H2 type LIVER10000870//Urocanase
 LIVER10001040//AMP-binding enzyme
 LIVER10002300//Respiratory-chain NADH dehydrogenase 51 Kd subunit
 LIVER10004330//Cyclic nucleotide-binding domain//Glutathione S-transferases//Uncharacterized protein family
 45 UPF0028
 LIVER10005420//Bowman-Birk serine protease inhibitor family
 LIVER20000330//Peptidase family M1//K+ channel tetramerisation domain
 LIVER20000370//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain
 MAMGL10000560//K-box region
 50 MAMGL10001780//Luminal portion of Cytochrome b559, alpha (gene psbE) subunit.
 MAMGL10001820//DIX domain
 MESAN10000350//Neurohypophyseal hormones, C-terminal Domain
 MESAN10001800//Sterol O-acetyltransferase
 MESAN20000920//SAM domain (Sterile alpha motif)//PDZ domain (Also known as DHR or GLGF)//Phosphatidylinositol 3- and 4-kinases
 55 MESAN20005010//PWWP domain
 NB9N41000470//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat

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- NT2R120016570//DnaJ central domain (4 repeats)
 NT2R120018480//Glutamine synthetase/Notch (DSL) domain/Notch (DSL) domain
 NT2R120018860//Immunoglobulin domain/SPRY domain
 NT2R120022020//Phosphatidylinositol-specific phospholipase C, X domain
 5 NT2R1200225170//PDZ domain (Also known as DHR or GLGF) //PDZ domain (Also known as DHR or GLGF).
 NT2R120025300//Ubiquitin family
 NT2R120025410//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Putative zinc finger in N-recogin//Zinc finger, C2H2
 type//Zinc finger, C2H2 type//Transcription factor S-II (TFIIS)//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zn-finger
 inubiquitin-hydrolases and other proteins//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc
 10 finger, C2H2 type
 NT2R120025540//TPR Domain//TPR Domain//TPR Domain
 NT2R120025850//jmyN domain//jmyC domain
 NT2R120029580//C2 domain//C2 domain
 NT2R120029700//EF hand//EF hand
 15 NT2R120030110//Immunoglobulin domain
 NT2R120031540//Interleukin-6/G-CSF/MGF family
 NT2R120032050//Armaddillo/beta-catenin-like repeats//Armaddillo/beta-catenin-like repeats
 NT2R120033440//PDZ domain (Also known as DHR or GLGF).
 NT2R120036780//Subtilase family//Protein convertase P-domain
 20 NT2R120036950//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine
 Rich Repeat//Leucine Rich Repeat//Insulin/GF/Relaxin family//Ribosomal RNA adenine dimethylases//SAM domain
 (Sterile alpha motif)//TFII alpha subunit//Zinc finger, C3HC4 type (RING finger)
 NT2R120037510//Formamidopyrimidine-DNA glycosylase
 NT2R120048080//K+ channel tetramerisation domain
 25 NT2R120049850//Domain of unknown function
 NT2R120050610//Peptidase family M1
 NT2R120050870//Voltage gated chloride channels//Xanthine/uracil permeases family//Sulfate transporter family//STAS
 domain
 NT2R120051500//Sialyltransferase family//Photosynthetic reaction center protein
 30 NT2R120053680//Zinc finger, C2H2 type
 NT2R120055840//Glutathione S-transferases//Protein of unknown function DUF61//Glutathione S-transferases.
 NT2R120056470//bZIP transcription factor//Transposase/bZIP transcription factor//Outer membrane efflux protein//
 Intermediate filament proteins
 NT2R120058110//Guanine nucleotide exchange factor for Ras-like GTPases; N-terminal motif//RasGEF domain
 35 NT2R120060710//Zinc finger, G2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//TRAF-type zinc finger//Zinc
 finger, C2H2 type//Zinc finger, C2H2 type
 NT2R120062100//Src homology domain 2
 NT2R120064120//Ras family//Cell division protein
 NT2R120066790//Immunoglobulin domain
 40 NT2R120067030//L1 (late) protein
 NT2R120067350//Zinc finger, G2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//TRAF-
 type zinc finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc
 finger, C2H2 type
 NT2R120068250//Dolichyl-phosphate-mannose-protein mannosyltransferase//S-adenosylmethionine synthetase
 45 NT2R120068550//Helicases conserved C-terminal domain
 NT2R120070480//Atrial natriuretic peptide
 NT2R120070840//Immunoglobulin domain
 NT2R120070960//Hydroxymethylglutaryl-coenzyme A reductase/RhoGEF domain//Hpt domain//PH domain
 NT2R120071330//KRAB box//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2
 50 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Transcription factor S-11 (TFIIS)//Zinc
 finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc
 finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc
 finger, C2H2 type
 NT2R120071480//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain,
 55 G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
 NT2R120072540//Ribosomal RNA adenine dimethylases//SAM domain (Sterile alpha motif)//TFII alpha subunit//Zinc
 finger, C3HC4 type (RING finger)
 NT2R120073840//Eukaryotic protein kinase domain

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- [illegible]

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NT2RP7002908//Oxyol-iron-binding protein/Hsp90 protein
NT2RP7003050//PHD-finger
NT2RP70032030//KRAB box/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/GATA zinc finger/
Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type
NT2RP70033040//Rhodanese-like domain/Integrase Zinc binding domain/Integrase Zinc binding domain/DnaJ central
domain (4 repeats)
NT2RP70036290//Glypican/Leucine Rich Repeat/Leucine Rich Repeat
NT2RP70036470//Porphyobilinogen deaminase/GHMP kinases putative ATP-binding proteins
NT2RP70036800//Methanol dehydrogenase beta subunit/BTB/POZ domain/Kelch motif/Kelch motif/Kelch motif/
Kelch motif/Kelch motif/Kelch motif
NT2RP70039600//Calpain inhibitor repeat
NT2RP70042040//PHD-finger/FYVE zinc finger/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/
Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type
NT2RP70042330//TPR Domain/TPR Domain/TPR Domain/TPR Domain/TPR Domain/TPR Domain/TPR Domain/TPR Domain
NT2RP70043960//SH3 domain/SH3 domain/SH3 domain/SH3 domain/SH3 domain/SH3 domain
NT2RP70045410//Helix-loop-helix DNA-binding domain
NT2RP70046580//PHD-finger/PHD-finger
NT2RP70046870//Macrophage migration inhibitory factor (MIF)/WD domain, G-beta repeat/WD domain, G-beta re-
peat/WD domain, G-beta repeat/WD domain, G-beta repeat/WD domain, G-beta repeat/Arenavirus glycoprotein//
WD domain, G-beta repeat
NT2RP70049150//PWFP domain
NT2RP70049250//WH1 domain
NT2RP70055020//Sigma-54 interaction domain/ATPases associated with various cellular activities (AAA)
NT2RP70055130//KRAB box/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/
Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/TRAF-type zinc
finger/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/DM DNA binding domain/Zinc finger, C2H2 type
NT2RP70061820//Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc
finger, C2H2 type/Zinc finger, C2H2 type
NT2RP70061880//GTPase-activator protein for Ras-like GTPase
NT2RP70062960//SNF2 and others N-terminal domain/SNF2 and others N-terminal domain/Leishmanolysin/Heli-
cases conserved C-terminal domain
NT2RP70063040//Plant PEC family metallothionein/Cell division protein
NT2RP70064900//KRAB box/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/
PHD-finger/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Transcription factor S-II (TFI-
IS)/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/
Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/
Zinc finger, C2H2 type/Zinc finger, C2H2 type
NT2RP70065270//LIM domain containing proteins/LIM domain containing proteins/LIM domain containing proteins//
Helper component proteinase
NT2RP70069860//KRAB box/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/
Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/
Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/
Putative zinc finger in N-recogin/Zinc finger, C2H2 type/DM DNA binding domain/Zinc finger, C2H2 type
NT2RP70071770//STAT protein/Zinc finger, C3HC4 type (RING finger)
NT2RP70072210//Viral (Superfamily 1) RNA helicase
NT2RP70072520//PAS domain/PAS domain/PAS domain/Eukaryotic protein kinase domain
NT2RP70074060//Glutamine synthetase
NT2RP70075370//Zinc finger, C3HC4 type (RING finger)/B-box zinc finger//CONSTANS family zinc finger//Putative
zinc finger in N-recogin//SPRY domain
NT2RP70076100//SAM domain (Sterile alpha motif)
NT2RP70076430//Apolipoprotein A1/A4/E family
NT2RP70079250//FS8 type C domain/Laminin G domain/Laminin G domain/EGF-like domain/Thrombospondin N-
terminal -like domains/Laminin G domain
NT2RP70079750//Laminin G domain
NT2RP70081370//Herpesvirus glycoprotein M/ABC transporter/Ribosomal S17
NT2RP70081440//Eukaryotic protein kinase domain
NT2RP70081670//Helix-hairpin-helix motif //S1 RNA binding domain

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[illegible]

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- C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/FYVE zinc finger/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Transcription factor S-II (TFIIS)/Zinc finger, C2H2 type/Zinc finger, C2H2 type
- OCBBF20011240//Glutathione S-transferases.
- 5 OCBBF20011400//WD domain, G-beta repeat//K+ channel tetramerisation domain//7-fold repeat in Clathrin and VPS
- OCBBF20011760//BTB/POZ domain/Kelch motif//Kelch motif//Kelch motif//Kelch motif//Kelch motif
- OCBBF20012100//PAP2 superfamily
- OCBBF20013070//Zinc finger, C2H2 type/Zinc finger, C2H2 type
- OCBBF20014940//JBA domain
- 10 OCBBF20015270//Zinc finger, C2H2 type/Bacterial type II secretion system protein
- OCBBF20015280//lactate/malate dehydrogenase
- OCBBF20015860//ATP synthase Alpha chain, C terminal
- PEBLM10000340//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)//Zn-finger in Ran binding protein and others.
- 15 PEBLM10000680//Actin
- PEBLM20001120//Thymidylate kinase//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat
- PEBLM20002480//KRAB box//Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type//TRAF-type zinc finger/Zinc finger, C2H2 type/Transcription factor S-II (TFIIS)/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type
- 20 PEBLM20002700//KRAB box//Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type
- PEBLM20003080//Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type
- 25 PEBLM20003950//SCAN domain
- PEBLM20004790//Src homology domain 2//Eukaryotic protein kinase domain
- PLACE50000370//7-fold repeat in Clathrin and VPS
- 30 PLACE50000580//Apolipoprotein A1/A4/E family
- PLACE50000680//Sushi domain (SCR repeat)//Sushi domain (SCR repeat)
- PLACE60002050//Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type
- PLACE60003790//Luminal portion of Cytochrome b559, alpha (gene psbE) subunit. PLACE60004290//Gag P30 core shell protein
- 35 PLACE60012810//AMP-binding enzyme
- PLACE60014430//moaA / nitB / pqqE family//MoaC family
- PLA0E60018850//Adenylate and Guanylate cyclase catalytic domain
- PLACE60021020//Integrase Zinc binding domain//Integrase Zinc binding domain/DnaJ central domain (4 repeats)
- PLACE60021510//KRAB box//Zinc finger, C2H2 type/Zinc finger, C2H2 type//Putative zinc finger in N-recognition/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type
- 40 PLACE60026680//Sorbin homologous domain//SH3 domain//SH3 domain
- PLACE60030380//Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type
- 45 PLACE60032040//Hirudin
- PLACE60037050//ENV polyprotein (coat polyprotein)
- PLACE60038500//Mitochondrial carrier proteins//Mitochondrial carrier proteins PLACE60044640//Small cytokines (interleukin/chemokine), interleukin-8 like
- PLACE60048630//Phorbol esters/diacylglycerol binding domain (C1 domain)//PHD-finger
- 50 PROST10003430//PHD-finger//Zinc finger, C3HC4 type (RING finger)//TRAF-type zinc finger//PDZ domain (Also known as DHR or GLGF)//PDZ domain (Also known as DHR or GLGF)//PDZ domain (Also known as DHR or GLGF)//PDZ domain (Also known as DHR or GLGF).
- PROST10005360//F5/8 type C domain//Laminin G domain//Laminin G domain//EGF-like domain//Fibrinogen beta and gamma chains, C-terminal globular domain
- 55 PROST20003250//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- PROST20018230//Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type
- PROST20018990//ADP-ribosylation factor family//Ras family
- PROST20023380//K+ channel tetramerisation domain//BTB/POZ domain

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PROST20029600/Small cytokines (intercrine/chemokine), interleukin-8 like//Immunoglobulin domain
 PROST20031170/Heavy-metal-associated domain//HECT-domain (ubiquitin-transferase).
 PROST20033380/TPR Domain//TPR Domain//TPR Domain
 PROST20033400/Eukaryotic protein kinase domain
 5 PROST20043320/Paramyxovirus nucleocapsid protein//SH3 domain
 PROST20044160/Tropomyosins
 PROST20051210/Protein phosphatase 2C//Protein phosphatase 2C
 PROST20064500/Sulfotransferase proteins
 PROST20067370/TRAF-type zinc finger//DnaJ central domain (4 repeats)
 10 PROST20069880/Atrial natriuretic peptide
 PROST20072890/K+ channel tetramerisation domain//BTB/POZ domain
 PROST20073170/K+ channel tetramerisation domain//BTB/POZ domain//Zinc finger, C2H2 type//Zinc finger, C2H2
 type//Zinc finger present in dystrophin, CBP/p300
 PROST20073890/Platelet-derived growth factor (PDGF)
 15 PROST20085160/Tropomyosins//Tropomyosins
 PROST20094830/PH domain
 PUAE10003220/Photosystem I reaction centre subunit VIII
 SALGL10000050/Permeases for cytosine/purines, uracil, thiamine, allantoin
 SALGL10000650/SAM domain (Sterile alpha motif)/Sterile alpha motif (SAM)/Pointed domain
 20 SALGL10001570/Collin pore forming domain//MotA/TolQ/ExbB proton channel family
 SKMUS10000140/Ubiquitin family//Ubiquitin family//Ubiquitin family//Ubiquitin family//Ubiquitin family
 SKMUS10000220/WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain,
 G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
 SKMUS10000640/Zinc finger, C3HC4 type (RING finger)//Zinc finger, C3HC4 type (RING finger)//PHD-finger//B-box
 25 zinc finger//3'5'-cyclic nucleotide phosphodiesterase
 SKMUS10001040/bZIP transcription factor
 SKMUS10001180/Coronavirus S2 glycoprotein
 SKMUS10001290/MutL-like domain
 SKMUS10001770/Protein-L-isoaspartate(D-aspartate) O-methyltransferase (PCMT) SKMUS20000740/ubI/COQ5
 30 methyltransferase family//Cyclopropane-fatty-acyl-phospholipid synthase
 SKMUS20001170/ATP synthase Alpha chain, C terminal//MAGE family
 SKMUS20002710/Hepatitis C virus capsid protein
 SKMUS20003900/Mov34/MPN/PAD-1 family
 SKMUS20004580/LIM domain containing proteins//Nebulin repeat//Nebulin repeat//Nebulin repeat//Nebulin repeat//
 35 Nebulin repeat//Nebulin repeat//Nebulin repeat//Nebulin repeat//Nebulin repeat
 SKMUS20007240/Thiamine pyrophosphate enzymes//Thiamine pyrophosphate enzymes//Thiamine pyrophosphate
 enzymes
 SKMUS20008630/OB-fold nucleic acid binding domain//tRNA synthetases class II (F)/tRNA synthetases class II (D,
 K and N)
 40 SKMUS20009540/F-box domain.
 SKMUS20011290/Iron-containing alcohol dehydrogenases//Iron-containing alcohol dehydrogenases
 SKMUS20013640/Laminin EGF-like (Domains III and V)
 SKMUS20016340/HMG (high mobility group) box
 SKMUS20018620/Ank repeat//Ank repeat//Glutamine amidotransferases class-III//Ank repeat
 45 SKMUS20018680/Phorbol esters/diacylglycerol binding domain (C1 domain)//CONSTANS family zinc finger//SH3 do-
 main
 SKNMC10000290/Zinc finger C-x8-C-x5-C-x3-H type (and similar).
 SKNMC10002510/ABC transporter transmembrane region//Phosphoribulokinase//ATPases associated with various
 cellular activities (AAA)/ABC transporter
 50 SKNMC20000650/Zinc finger, C2H2 type//Protein phosphatase 2C//Zinc finger, C2H2 type//Zinc finger, C2H2 type//
 Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 SKNMC20000970/RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)//Elongation factor TS//Protein-L-iso-
 aspartate(D-aspartate) O-methyltransferase (PCMT)/Met-10+ like proteins
 SKNMC20002240/KRAB box//Zinc finger, C2H2 type//LIM domain containing proteins//Zinc finger, C2H2 type//TRAF-
 55 type zinc finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//LIM
 domain containing proteins//PHD-finger//Zinc finger, C2H2 type
 SKNMC20003580/Helix-loop-helix DNA-binding domain
 SKNMC20010570/F-box domain.

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SKNMC20015030//Keratin, high sulfur B2 protein
SKNMC20015960//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//
Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Bacterial stress protein//Ank re-
peat//Formylmethanofuran—tetrahydromethanopterin formyltransferase//Ank repeat//Ank repeat//Ank repeat//Neu-
5 raxin and MAP1B proteins//FYVE zinc finger
SKNSH10001740//Pyridoxal-dependent decarboxylase
SKNSH10003010//SH3 domain
SKNSH20003470//Heme-binding domain in cytochrome b5 and oxidoreductases
SMINT10000160//UDP-glucuronosyl and UDP-glucosyl transferases
10 SMINT10000420//Cytochrome oxidase subunit II//ABC transporter//Biotin-dependent aromatic amino acid hydrox-
ylase
SMINT10000570//Immunoglobulin domain//Immunoglobulin domain//Immunoglobulin domain
SMINT10000710//Immunoglobulin domain
SMINT10001030//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//Ank repeat//
15 Ank repeat//Ank repeat
SMINT20002270//Disintegrin//Trans-activation protein X
SMINT20002770//Transcriptional regulatory protein, C terminal//Immunoglobulin domain
SPLEN10001430//HMG (high mobility group) box
SPLEN20000720//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//TRAF-type zinc finger//Zinc
20 finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
SPLEN20001340//Peptidase family M20/M25/M40
SPLEN20001970//Transcription factor TFIIH repeat
SPLEN20002670//WD domain, G-beta repeat
SPLEN20003670//RasGEF domain//Ras association (RalGDS/AF-6) domain
25 STOMA10001860//Cytosolic long-chain acyl-CoA thioester hydrolase//OB-fold nucleic acid binding domain//Cytosolic
long-chain acyl-CoA thioester hydrolase
STOMA20000880//Immunoglobulin domain
STOMA20001210//Cys/Met metabolism PLP-dependent enzyme//Aminotransferases class-I
STOMA20002670//MgC family
30 STOMA20002890//Adaptin N terminal region
STOMA20003960//LIM domain containing proteins//LIM domain containing proteins STOMA20004820//PH domain//
EF hand//EF hand//Phosphatidylinositol-specific phospholipase C, X domain
SYNOV10001280//Lipoate-protein ligase B
SYNOV20013740//KRAB box//Bacterial type II secretion system protein I/J//Zinc finger, C2H2 type//Zinc finger, C2H2
35 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2
type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
SYNOV20014510//SRF-type transcription factor (DNA-binding and dimerisation domain)
SYNOV20016480//glycosyl transferase family
TEST10000420//K-box region//Penicillin amidase
40 TEST10000510//Transient receptor
TEST10000550//Homeobox domain
TEST10000640//K+ channel tetramerisation domain//BTB/POZ domain//Kelch motif//Kelch motif//Kelch motif//Kelch
motif//Kelch motif
TEST10000700//Ubiquitin carboxyl-terminal hydrolases family 2//Ubiquitin carboxyl-terminal hydrolase family 2
45 TEST10001270//PLAT/LH2 domain//PLAT/LH2 domain//PLAT/LH2 domain
TEST10001380//Subtilase family//Protein convertase P-domain
TEST10001680//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine Rich Repeat//Leucine
Rich Repeat//Leucine Rich Repeat
TEST10001200//KRAB box
50 TEST10001540//Eukaryotic protein kinase domain
TEST10001770//von Willebrand factor type A domain//Protein convertase P-domain
TEST10002070//NifU-like N terminal domain
TEST10002380//Exonuclease//3'-5' exonuclease
TEST10002530//Ubiquitin family
55 TEST10003660//Tubulin//FtsZ family
TEST10005910//Adenylate kinase//Elongation factor Tu family//Adenylate kinase//6-phosphofructo-2-kinase//Shiki-
mate kinase//pKID domain//Adenylate kinase//Thymidylate kinase//AT Pases associated with various cellular activities
(AAA)

TEST120006000//Ank repeat//CAP-Gly domain

repeats//Armadillo/beta-catenin-like repeats//Armadillo/beta-catenin-like repeats
TESTI20031300//TPR Domain
TESTI20031520//mRNA capping enzyme
TESTI20031960//WD domain, G-beta repeat
TESTI20032280//Myb-like DNA-binding domain
TESTI20033250//UBX domain/Orotidine 5'-phosphate decarboxylases
TESTI20033270//DM DNA binding domain
TESTI20033540//Zinc finger, C2H2 type
TESTI20033560//F-box domain.
TESTI20034190//ATP synthase Alpha chain, C terminal//AMP-binding enzyme
TESTI20034980//RhoGEF domain
TESTI20035120//C2 domain/Kinesin motor domain
TESTI20035510//NOL1/NOP2/sun family
TESTI20035890//UBA domain/Zinc finger C-x8-C-x5-C-x3-H type (and similar).
TESTI20036250//TSC-2/dip/bun family//NAD dependent epimerase/dehydratase family//Adenylate kinase/ATPases associated with various cellular activities (AAA)
TESTI20037810//Eukaryotic protein kinase domain
TESTI20038940//IQ calmodulin-binding motif/IQ calmodulin-binding motif//IO calmodulin-binding motif
TESTI20040000//short chain dehydrogenase//3-beta hydroxysteroid dehydrogenase/isomerase family
TESTI20040310//Domain of unknown function DUF84
TESTI20041220//VPR/VPX protein
TESTI20042870//ET module
TESTI20042950//3'5'-cyclic nucleotide phosphodiesterase/Peptidase family M1
TESTI20049820//Cyclic nucleotide-binding domain
TESTI20053960//KRAB box/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/transcription factor S-II (TFIIIS)/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/TRAF-type zinc finger/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Porboral esters/diaclyglycerol binding domain (C1 domain)//Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type
TESTI20055840//PH domain//PH domain
TESTI20056900//Urease, gamma subunit//IQ calmodulin-binding motif/IQ calmodulin-binding motif
TESTI20057310//Tropomyosins
TESTI20057420//Acyl CoA binding protein/Ribosomal Protein L2
TESTI20064830//Tetrahydrofolate dehydrogenase/cyclohydrolase
TESTI20068660//Domain of unknown function DUF19//TPR Domain//TPR Domain//TPR Domain
TESTI20068720//Zinc finger, C2H2 type/Zinc finger, C2H2 type
TESTI20074640//KRAB box/Zinc finger, C2H2 type/MYND finger/Zinc finger, C2H2 type/Zinc finger, C2H2 type/
Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/
Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type TESTI20074660//KRAB box/Zinc finger, C2H2
type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2
type/Zinc finger, C2H2 type/PHD-finger/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc finger, C2H2 type/Zinc
finger, C2H2 type/MYND finger/Zinc finger, C2H2 type
TESTI20074800//Glycan
TESTI20077490//Signal peptidase (SPase) II
TESTI20078640//SCAN domain
TESTI20078720//ATP synthase B/B' CF(0)/Ribosomal L29 protein TESTI20079510//Immunoglobulin domain//mmu-
noglobulin domain//Adenovirus E3 region protein CR1//Immunoglobulin domain//Immunoglobulin domain//Fbronectin
type III domain//Fibronectin type III domain
TESTI20080200//MitB family UPF0032
TESTI20080330//Ribosomal protein L14p/L23e
TESTI20083430//TPR Domain
TESTI20083870//EF hand//EF hand//Phosphatidylinositol 3- and 4-kinases//EF hand
TESTI20086570//MAGE family
TESTI20087740//TPR Domain//TPR Domain//Outer membrane efflux protein/TPR Domain//TPR Domain
TESTI20138320//Transketolase
TESTI20140360//metallopeptidase family M24
TESTI20177440//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat

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THYMU10000830//FAD binding domain
 THYMU10001760//Immunoglobulin domain
 THYMU10002910//Adaptin N terminal region
 THYMU10003590//PH domain/RhoGAP domain
 5 THYMU10004590//HMG (high mobility group) box
 THYMU10005580//Synaptobrevin
 THYMU20002380//Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)
 THYMU20003690//Prokaryotic DNA topoisomerase//Protein of unknown function DUF122//Eukaryotic protein kinase domain
 10 TRACH1 0000740//Immunoglobulin domain//Immunoglobulin in domain//Immunoglobulin domain//Immunoglobulin domain
 TRACH1 0001250//Immunoglobulin domain//Immunoglobulin in domain//Immunoglobulin domain//Immunoglobulin domain
 TRACH20000150//Fatty acid desaturase//Protein phosphatase 2C
 15 TRACH20001850//Molluscan rhodopsin C-terminal tail
 TRACH20002370//KRAB box//Zinc finger, C2H2 type//FYVE zinc finger//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 TRACH20002500//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat//WD domain, G-beta repeat
 20 TRACH20002890//PH domain//Src homology domain 2
 TRACH20003930//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
 TRACH20004110//Zinc finger, C2H2 type
 TRACH20004200//Neurohypophyseal hormones, C-terminal Domain//Keratin, high sulfur B2 protein
 25 TRACH20004720//Aminotransferases class-III//Aminotransferases class-I
 TRACH20004960//AMP-binding enzyme
 TRACH20006650//LacY proton/sugar symporter//Sugar (and other) transporter
 TRACH20006750//E1 Protein, N terminal domain//ATP synthase (E/31 kDa) subunit TRACH20009260//short chain dehydrogenase
 30 TRACH20012890//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
 TRACH20016070//Adenylate cyclase
 UMVN10001220//Corticotropin-releasing factor family
 UMVN20001330//C2 domain//C2 domain//C2 domain
 UTERU1 0001600//SCAN domain//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 35 C2H2 type//Zinc finger, C2H2 type//Zinc finger, C2H2 type
 UTERU1 0001920//Integrase core domain

EXAMPLE 640 **Functional categorization based on the full-length nucleotide sequences**

[0209] The functional prediction and categorization of the proteins encoded by the clones were carried out based on the result of homology search of the databases of GenBank, Swiss-Prot, UniGene and nr (see the Homology Search Result Data) for the full-length nucleotide sequences and the result of domain search of the amino acid sequences
 45 deduced from the full-length nucleotide sequences (see Example 5).

[0210] The clone predicted to belong to the category of secretory protein/membrane protein means a clone having hit data with some annotation, such as growth factor, cytokine, hormone, signal, transmembrane, membrane, extra-cellular matrix, receptor, G-protein coupled receptor, ionic channel, voltage-gated channel, calcium channel, cell adhesion, collagen, connective tissue, etc., suggesting that it is a secretory or membrane protein, or means a clone in
 50 which the presence of nucleotide sequence encoding a signal sequence or transmembrane domain was suggested by the results of PSORT and SOSUI analyses for deduced ORF.

[0211] The clone predicted to belong to the category of glycoprotein-related protein means a clone having hit data with some annotation, such as glycoprotein, suggesting that the clone encodes a glycoprotein-related protein.

[0212] The clone predicted to belong to the category of signal transduction-related protein means a clone having hit data with some annotation, such as serine/threonine-protein kinase, tyrosine-protein kinase, SH3 domain, SH2 domain, etc., suggesting that the clone encodes a signal transduction-related protein.

[0213] The clone predicted to belong to the category of transcription-related protein means a clone having hit data with some annotation, such as transcription regulation, zinc finger, homeobox, etc., suggesting that the clone encodes

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a transcription-related protein.

[0214] The clone predicted to belong to the category of disease-related protein means a clone having hit data with some annotation, such as disease mutation, syndrome, etc., suggesting that the clone encodes a disease-related protein, or means a clone whose full-length nucleotide sequence has hit data for Swiss-Prot, GenBank, or UniGene, where the hit data corresponds to genes or proteins which have been deposited in the Online Mendelian Inheritance in Man (OMIM) (<http://www.ncbi.nlm.nih.gov/omim/>), which is the human gene and disease database.

[0215] The clone predicted to belong to the category of enzyme and/or metabolism-related protein means a clone having hit data with some annotation, such as metabolism, oxidoreductase, E. C. No. (Enzyme commission number), etc., suggesting that the clone encodes an enzyme and/or metabolism-related protein.

[0216] The clone predicted to belong to the category of cell division and/or cell proliferation-related protein means a clone having hit data with some annotation, such as cell division, cell cycle, mitosis, chromosomal protein, cell growth, apoptosis, etc., suggesting that the clone encodes a cell division and/or cell proliferation-related protein.

[0217] The clone predicted to belong to the category of cytoskeleton-related protein means a clone having hit data with some annotation, such as structural protein, cytoskeleton, actin-binding, microtubules, etc., suggesting that the clone encodes a cytoskeleton-related protein.

[0218] The clone which is predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein means a clone having hit data with some annotation, such as nuclear protein, RNA splicing, RNA processing, RNA helicase, polyadenylation, etc., suggesting that the clone encodes a nuclear protein and/or RNA synthesis-related protein.

[0219] The clone predicted to belong to the category of protein synthesis and/or transport-related protein means a clone having hit data with some annotation, such as translation regulation, protein biosynthesis, amino-acid biosynthesis, ribosomal protein, protein transport, signal recognition particle, etc., suggesting that the clone encodes a protein synthesis and/or transport-related protein.

[0220] The clone predicted to belong to the category of cellular defense-related protein means a clone having hit data with some annotation, such as heat shock, DNA repair, DNA damage, etc., suggesting that the clone encodes a cellular defense-related protein.

[0221] The clone predicted to belong to the category of development and/or differentiation-related proteins means a clone having hit data with some annotation, such as developmental protein, etc., suggesting that the clone encodes a development and/or differentiation-related protein.

[0222] The clone predicted to belong to the category of DNA-binding and/or RNA-binding protein means a clone having hit data with some annotation, such as DNA-binding, RNA-binding, etc.

[0223] The clone predicted to belong to the category of ATP-binding and/or GTP-binding protein means a clone having hit data with some annotation, such as ATP-binding, GTP-binding, etc.

[0224] In this functional categorization, when a single clone corresponded to multiple categories of those shown above, the clone was assigned to the multiple categories. However, the function of a protein is not restricted to the functional category in this classification, and there is the possibility that other functions are newly assigned to the protein.

[0225] The clones predicted to belong to the category of secretory protein and/or membrane protein are the following 439 clones.

3NB6910000180, 3NB6910000850, 3NB6920000290, 3NB6920003300, 3NB6920005450, 3NB6920010020, 4ADRL10000180, 4ADRL10001600, 4ADRL20003230, 4BGG120010670, 4BNGH410000340, 4BNGH410001040, 4BNGH410001180, 4BNGH410001370, 4BNGH410001980, 4BRACE10000730, 4BRACE10001690, 4BRACE20002800, 4BRACE20007180, 4BRACE20010650, 4BRACE20011170, 4BRACE20011430, 4BRACE20013400, 4BRACE20013520, 4BRACE20014230, 4BRACE20014530, 4BRACE20014920, 4BRACE20015080, 4BRACE20018590, 4BRACE20022270, 4BRACE20024680, 4BRACE20026350, 4BRACE20026850, 4BRACE20030780, 4BRACE20031100, 4BRACE20034490, 4BRACE20071380, 4BRACE20071970, 4BRACE20072810, 4BRACE20074010, 4BRACE20074470, 4BRACE20075020, 4BRACE20075380, 4BRACE20076410, 4BRACE20076630, 4BRACE20076850, 4BRACE20077610, 4BRACE20077640, 4BRACE20077980, 4BRACE20078680, 4BRACE20079530, 4BRACE20084430, 4BRACE20086550, 4BRACE20089600, 4BRACE20091880, 4BRAWH10000010, 4BRAWH10000370, 4BRAWH10000940, 4BRAWH10001620, 4BRAWH10001800, 4BRAWH20001090, 4BRAWH20004430, 4BRAWH20006970, 4BRAWH20009840, 4BRAWH20011290, 4BRAWH20011410, 4BRAWH20011680, 4BRAWH20014380, 4BRAWH20014840, 4BRAWH20015030, 4BRAWH20036930, 4BRAWH20038320, 4BRAWH20040950, 4BRAWH20052250, 4BRAWH20059980, 4BRAWH20087060, 4BRAWH20092610, 4C034C20000510, 4CTONG20013660, 4CTONG20015330, 4CTONG20028160, 4CTONG20037820, 4CTONG20047160, 4DFNES20003350, 4FCBBF10006180, 4FCBBF10006750, 4FCBBF20005910, 4FCBBF20007330, 4FCBBF20008150, 4FCBBF20009400, 4FCBBF20015380, 4FEBRA20003780, 4FEBRA20004040, 4FEBRA20004150, 4FEBRA20004520, 4FEBRA20004910, 4FEBRA20006560, 4FEBRA20006930, 4FEBRA20007330, 4FEBRA20008090, 4FEBRA20008800, 4FEBRA20010930, 4FEBRA20012270, 4FEBRA20012450, 4FEBRA20012940, 4FEBRA20013510, 4FEBRA20014870, 4FEBRA20014920, 4FEBRA20015840, 4FEBRA20020860, 4FEBRA20021910, 4FEBRA20025250, 4FEBRA20031550, 4FEBRA20037070, 4FEBRA20041100, 4FEBRA20041910, 4FEBRA20057780, 4FEBRA20063150, 4FEBRA20066670, 4FEBRA20067930,

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HCASM10000610, HCASM200002020, HEART20000990, HEART20004920, HHDP20000950, HLUNG10000240, HLUNG10000370, HLUNG10001100, HLUNG20001160, HLUNG20001250, HLUNG20001420, HLUNG20001760, HLUNG20002550, HSYRA200003470, HSYRA200006290, HSYRA200008280, HSYRA200011030, HSYRA200013320, HSYRA200014200, HSYRA200015800, IMR3210000440, IMR3210001580, IMR3210002660, IMR3220007750, 5 IMR32200008590, IMR32200009840, IMR32200014350, KIDNE10000080, KIDNE10001040, KIDNE10001430, KIDNE20000700, KIDNE200000850, KIDNE20001670, KIDNE20003150, KIDNE20003300, KIDNE20003490, KIDNE20004220, KIDNE20005170, KIDNE20005190, KIDNE200033050, KIDNE20033570, KIDNE20039410, KIDNE20042620, KIDNE20042950, KIDNE20044110, KIDNE20048280, KIDNE20049810, KIDNE20054000, KIDNE20054770, KIDNE20060530, KIDNE20060620, KIDNE20063530, KIDNE20063760, KIDNE20066520, 10 KIDNE20067800, KIDNE20071860, KIDNE20073520, KIDNE20074220, KIDNE20075690, LIVER10000580, LIVER10000670, LIVER10001040, LIVER10001110, LIVER10001750, LIVER10005420, LIVER20004160, MAMGL10000320, MAMGL10001840, MESAN10000350, MESAN10001470, MESAN10001800, MESAN20001490, NB9N420000420, NHNCP20002060, NT2NE10000230, NT2NE10000830, NT2NE10001630, NT2NE20003270, NT2NE20003920, NT2NE20004550, NT2RE20004700, NT2NE20005500, NT2NE20012470, NT2NE20014350, 15 NT2NE20016260, NT2NE20034080, NT2NE20047160, NT2NE20055170, NT2NE20057200, NT2R120005970, NT2R120009740, NT2R12001100, NT2R120014490, NT2R120015400, NT2R120015950, NT2R120016570, NT2R120018660, NT2R120020220, NT2R120021520, NT2R120022430, NT2R120022520, NT2R120025300, NT2R120030110, NT2R120030510, NT2R12003310, NT2R120033830, NT2R120036780, NT2R120042840, NT2R120044420, NT2R120049850, NT2R120050870, NT2R120051500, NT2R120066820, 20 NT2R120068250, NT2R120070480, NT2R120070840, NT2R120073030, NT2R120074980, NT2R120077540, NT2R120078270, NT2R120080500, NT2R120081880, NT2R120084810, NT2R120085980, NT2R120089420, NT2R120092890, NT2R120095070, NT2RP60000320, NT2RP60000390, NT2RP60001090, NT2RP70000690, NT2RP70002380, NT2RP70002590, NT2RP70003640, NT2RP70011660, NT2RP70015910, NT2RP70021510, NT2RP70023760, NT2RP70023790, NT2RP70028190, NT2RP70029820, NT2RP70040800, NT2RP70043730, 25 NT2RP70047900, NT2RP70049250, NT2RP70055200, NT2RP70064080, NT2RP70071540, NT2RP70071770, NT2RP70073810, NT2RP70074220, NT2RP70075040, NT2RP70076170, NT2RP70079250, NT2RP70079750, NT2RP70081330, NT2RP70081730, NT2RP70083150, NT2RP70085500, NT2RP70090120, NT2RP70091490, NT2RP70091680, NT2RP70092360, NT2RP70093220, NT2RP70093730, NT2RP70094920, NT2RP70094810, NT2RP70094980, NT2RP70095070, NTONG10000980, NTONG10002140, NTONG10002570, NTONG20002650, 30 NTONG20004920, NTONG20008000, NTONG20012220, OCBBF10000420, OCBBF20002310, OCBBF20009980, OCBBF20012100, PANCE100000210, PLACE50000670, PLACE50000680, PLACE500001050, PLACE50001130, PLACE60012810, PLACE60018860, PLACE6002160, PLACE60020840, PLACE60025990, PLACE60037050, PLACE60037450, PLACE60043960, PLACE60044540, PLACE60047380, PLACE60049930, PLACE60050290, PROST10002200, PROST10002720, PROST10005260, PROST10005360, PROST20000360, PROST20026820, 35 PROST20029600, PROST20032320, PROST20033020, PROST20039220, PROST20044160, PROST20051430, PROST20054260, PROST20055800, PROST20059190, PROST20059430, PROST20069860, PROST20072370, PROST20073890, PUAEN10000570, PUAEN10003220, SALGL10001570, SKMUS20007740, SKNMC10000190, SKNMC10000290, SKNMC10002290, SKNMC10002510, SKNMC20011130, SKNMC20015030, SMINT10000180, SMINT10000420, SMINT10000570, SMINT10001180, SMINT20000180, SMINT20002770, SPLEN10000910, SPLEN20001340, SPLEN20002430, SPLEN20002700, SPLEN20003100, SPLEN20004960, STOMA10000520, 40 STOMA10001170, STOMA200003320, STOMA20002570, SYNVO20001770, SYNVO20016480, TEST10000420, TEST10000960, TEST10001270, TEST10001380, TEST10001770, TEST10006000, TEST10007620, TEST10008830, TEST10009090, TEST10009700, TEST10011340, TEST10012370, TEST10013520, TEST10014200, TEST10016210, TEST10016710, TEST10018520, TEST10018620, TEST10020020, 45 TEST100200810, TEST10022510, TEST10024230, TEST10024650, TEST10024670, TEST10025800, TEST10026320, TEST10026980, TEST10027000, TEST10027070, TEST10028660, TEST10030370, TEST10031930, TEST10034190, TEST10036490, TEST10039980, TEST10042870, TEST10047120, TEST10049940, TEST10056900, TEST10057420, TEST10058600, TEST10067740, TEST10069780, TEST10074800, TEST10077490, TEST10079510, TEST10080200, TEST10081440, TEST10087740, 50 TEST10088470, TEST10136910, THYMU10000830, THYMU10001760, THYMU10003290, THYMU10003820, THYMU10005580, TRACH10000630, TRACH10001000, TRACH10001400, TRACH20001850, TRACH20001960, TRACH20004200, TRACH20004960, TRACH20006650, TRACH20007670, TRACH20008980, TRACH20015920, UMVEN20001330, UTERU10000770, UTERU10000960, UTERU10001920, UTERU20000470, UTERU20003930, UTERU20004850

[0226] The clones predicted to belong to the category of glycoprotein-related protein are the following 87 clones.
 BNGH410000340, BNGH410001180, BRACE20014920, BRACE20015080, BRACE20018590, BRACE20024680, BRACE20026350, BRACE20031100, BRACE20074470, BRAWH10000370, BRAWH20001090, BRAWH20011660, BRAWH20014840, BRAWH20059980, CD34C20000510, CTONG20013660, CTONG20028160, CTONG20037820,

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FCBBF20007330, FEBRA20007330, FEBRA20008800, FEBRA20014920, FEBRA20015840, FEBRA20057780, HEART20005060, HLUNG10001100, HLUNG20002550, HSYRA20013320, IMR3210002660, IMR3220007750, KIDNE20003320, KIDNE20044110, KIDNE20063760, KIDNE20067600, KIDNE20073520, LIVER20000370, MESAN10000350, NT2NE10000830, NT2NE10001850, NT2NE20003270, NT2NE20016260, NT2RI20018660, NT2RI20025300, NT2RI20036780, NT2RI20077540, NT2RI20080500, NT2RI20085980, NT2RI20089420, NT2RI20092890, NT2RP70004670, NT2RP70005520, NT2RP70081370, NT2RP70083150, NT2RP70091490, NT2RP70092360, NT2RP70094980, NTONG10002140, OCBBF20002310, OCBBF20002770, PLACE50000680, PLACE50001130, PLACE60018860, PLACE60044540, PROST20018230, PROST20032320, PROST20073890, SALGL10001570, SKNMC20015030, SMINT10000160, SMINT20002770, SPLEN20001340, TEST110001270, TEST110001380, TEST120001770, TEST120024230, TEST120027070, TEST120036490, TEST120039980, TEST120057420, TEST120079510, THYMU10001760, TRACH10000740, TRACH10001250, TRACH20004200, UTERU20000470

[0227] The clones predicted to belong to the category of signal transduction-related protein are the following 46 clones.

ADRLG10000740, ASTRO10000180, BRACE20005770, BRACE20022020, BRACE20027360, BRACE20027920, BRAWH20006860, CTONG20005890, FEBRA20000350, HHDP20000550, IMR3220003020, KIDNE20033730, KIDNE20040840, KIDNE20053360, KIDNE20062990, NT2RI20033440, NT2RI20058110, NT2RI20062100, NT2RI20073840, NT2RP70006240, NT2RP70043960, NT2RP70046870, NT2RP70061880, NT2RP70072520, NT2RP70081440, NT2RP70083700, NTONG10001820, PEBLM20004790, PLACE60026680, PROST20033400, PROST20043320, SKMUS20000220, SKMUS20016680, SPLEN20003570, TEST120001540, TEST120005910, TEST120022560, TEST120024980, TEST120029120, TEST120034980, TEST120049820, TEST120055840, THYMU10003590, THYMU20003690, TRACH20002500, TRACH20002890

[0228] The clones predicted to belong to the category of transcription-related protein are the following 140 clones.

3NB6920010220, 3NB6920015110, 3NB6920015570, ADRLG10000650, BGGI120006840, BGGI120006930, BGGI120017140, BNGH410000800, BNGH420005320, BRACE10000930, BRACE20014550, BRACE20018550, BRACE20020910, BRACE20024090, BRACE20071740, BRAWH10000020, BRAWH10001640, BRAWH10001680, BRAWH20006330, BRAWH20009010, CTONG20025580, CTONG20028200, FCBBF10005980, FCBBF20000940, FCBBF20009510, FCBBF50002610, FEBRA20003970, FEBRA20003990, FEBRA20004540, FEBRA20009720, FEBRA20011460, FEBRA20017150, FEBRA20050140, FEBRA20064760, FEBRA20067360, FEBRA20069420, FEBRA20072800, HLUNG10000760, HLUNG20000680, HSYRA10001370, HSYRA20016310, IMR3210002420, IMR3220007420, KIDNE20000510, KIDNE20039940, KIDNE20061490, KIDNE20078110, NESOP10000870, NHNPC10001240, NHNPC20002120, NT2NE20002590, NT2NE20008090, NT2RI20003410, NT2RI20004120, NT2RI20004210, NT2RI20010830, NT2RI20018460, NT2RI20025410, NT2RI20025850, NT2RI20060710, NT2RI20067350, NT2RI20071330, NT2RI20074390, NT2RI20078790, NT2RI20087140, NT2RI20090650, NT2RI20092150, NT2RP60001000, NT2RP60001270, NT2RP70002710, NT2RP70008120, NT2RP70018560, NT2RP70024500, NT2RP70032030, NT2RP70036290, NT2RP70042040, NT2RP70045410, NT2RP70046560, NT2RP70055130, NT2RP70061620, NT2RP70062960, NT2RP70064900, NT2RP70069860, NT2RP70075370, NT2RP70085570, NT2RP70087200, NT2RP70090190, NTONG20003340, NTONG20003630, NTONG20015500, OCBBF20011010, OCBBF20011240, OCBBF20015860, PEBLM20002480, PEBLM20002700, PEBLM20003080, PEBLM20003950, PLACE60002050, PLACE60005550, PLACE60021510, PLACE60030380, PROST20018230, PROST20031170, PROST20073170, PUAEN10001610, SALGL10000650, SKMUS20000640, SKMUS20014920, SKNMC20000650, SKNMC20002240, SKNMC20003560, SMINT10001000, SMINT20005450, SPLEN20000220, SPLEN20000720, SYNOV200101340, SYNOV20013740, SYNOV20014510, TEST11000050, TEST120001200, TEST120007070, TEST120010490, TEST120015560, TEST120018150, TEST120018790, TEST120021490, TEST120026760, TEST120027890, TEST12003071, TEST120034130, TEST120042290, TEST120053960, TEST120074640, TEST120074660, TEST120078640, THYMU10004590, TRACH20000790, TRACH20002370, TRACH20009440, UTERU10001800

[0229] The clones predicted to belong to the category of disease-related protein are the following 219 clones. Further, hit data of all the clones for Swiss-Prot, or GenBank, UniGene, or nr corresponded to genes or proteins which had been deposited in the Online Mendelian Inheritance in Man (OMIM), which is the human gene and disease database, (the OMIM Number is shown in the parenthesis after the Clone Name).

ADRLG10000020 (605332), ADRLG10001600 (201910), ADRLG20000740 (300118), ASTRO200004170 (605937), BGGI120006840 (604480), BGGI120010970 (602346), BGGI120017140 (194631), BNGH410001770 (146690), BNGH420005320 (601260), BRACE10001870 (157132), BRACE20006980 (106410), BRACE20007180 (114160),

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- BRACE20014550 (140580), BRACE20018550 (109580), BRACE20018590 (602844), BRACE20027550 (179715),
BRACE20027720 (138760), BRACE20076850 (605209), BRACE20086550 (603540), BRAWH1000020 (605678),
BRAWH10001640 (606043), BRAWH20001770 (138450), BRAWH20005030 (179715), BRAWH20005220 (603747),
BRAWH20006330 (194500), BRAWH20006860 (602958), BRAWH20009840 (601258), BRAWH20011660 (230500):
230600,230650,253010), CD34C20000510 (600031), CTONG20005890 (603583), CTONG200019110 (603486),
CTONG200024180 (602895), CTONG20025580 (601856), CTONG20037820 (602729), CTONG20055530 (106410),
FCBBF20000340 (601408), FCBBF200009510 (194531), FCBBF40002820 (130410), FEBRA20001050 (600025),
FEBRA20003990 (601781),
FEBRA20004150 (128650,214700), FEBRA20004540 (194558), FEBRA20009720 (602277), FEBRA20010930
10 (603878), FEBRA20011460 (603900), FEBRA20050790 (176879), FEBRA20057880 (604362), FEBRA20064780
(602277), FEBRA20067930 (602911), FEBRA20070170 (606098), FEBRA20075510 (179513), FEBRA20075680
(179715), HCASM20002140 (123834), HEART20004480 (191045;115195), HLUNG10001050 (310400),
HLUNG20000680 (300024), HSYRA10001370 (602277), HSYRA20006400 (601278), HSYRA20013320 (146732),
HSYRA20016310 (604080),
15 IMR3210000440 (601890), IMR3220007910 (313440), KIDNE10001040 (603217), KIDNE20003150 (602417),
KIDNE20033730 (605216), KIDNE20042950 (120180), KIDNE20044110 (605239), KIDNE20050420 (214500),
KIDNE20059080 (604276), KIDNE20063760 (231950), KIDNE20078110 (603430), LIVER10002300 (161015),
LIVER10004330 (603197), LIVER20000330 (191161), LIVER20000370 (138670), MAMGL10001780 (603403),
MESAN100001800 (606048), MESAN20002910 (142810), MESAN20005010 (602769), NB9N410001350 (179508),
20 NHNPC10000840 (604819), NHNPC20002120 (194558), NT2NE10000730 (601905), NT2NE20002990 (147625),
NT2NE20003690 (232000), NT2NE20005170 (603330), NT2NE20005360 (150370), NT2NE20006580 (605969),
NT2NE20008090 (603899), NT2NE20013720 (180480), NT2NE20016340 (602184), NT2NE20055170 (128100),
NT2RI20004120 (600140), NT2RI20004210 (314997), NT2RI20010910 (601940), NT2RI20014500 (190370),
NT2RI20020410 (168730,180990), NT2RI20029580 (605689), NT2RI20031540 (300061), NT2RI20033440 (601014),
25 NT2RI20041900 (179715), NT2RI20056470 (123940), NT2RI20057230 (601940), NT2RI20067030 (603577),
NT2RI20070960 (311030), NT2RI20074980 (603105), NT2RI20077540 (300112), NT2RI20080590 (142461),
NT2RI20083960 (605612), NT2RI20084810 (603099), NT2RI20092150 (600834), NT2RI20092890 (603104),
NT2RP60000350 (605612), NT2RP60001000 (314995), NT2RP60001230 (600025), NT2RP70000890 (158340),
113720), NT2RP70004250 (160776), NT2RP70028750 (179838), NT2RP70029060 (140571), NT2RP70032030
30 (602277),
NT2RP70036290 (600005,209920), NT2RP70042600 (160776), NT2RP70046560 (602401), NT2RP70049250
(601703), NT2RP70055020 (604581), NT2RP70062960 (133540), NT2RP70063040 (604061), NT2RP70065270
(300111), NT2RP70069860 (602277), NT2RP70071770 (603046), NT2RP70073810 (601439), NT2RP70074220
(313440), NT2RP70075370 (109092), NT2RP70079250 (602346), NT2RP70081440 (601335), NT2RP70090120
35 (602277), NT2RP70090190 (194558), NT2RP70093220 (300008;300009;310468), NT2RP70094980 (135820),
NTONG10002460 (600856),
NTONG20003630 (600140), NTONG20015500 (604077), OCBBF10001180 (191161), OCBBF20008240 (187790),
PEBLM10000340 (133450), PEBLM20002480 (300024), PEBLM20003080 (604077), PEBLM20003950 (600834),
PLACE60000800 (607179), PLACE60002050 (600013), PLACE60003390 (603403), PLACE60014430 (603707),
40 PROST10001670 (313440), PROST10005360 (602346), PROST20002730 (601985;188550), PROST20032320
(253220), PROST20033400 (300203), PROST20062600 (601940), PROST20072890 (191161), PROST20073890
(192240),
PROST20085160 (191030;164970), SALGL10001570 (603743), SKMUS10000140 (191340), SKMUS10001180
(601402), SKMUS10001290 (604055), SKMUS20000740 (605196), SKMUS20003900 (604850), SKMUS20007240
45 (604300), SKMUS20016340 (163906), SKNMC10002510 (605452), SKNMC20000650 (604078), SKNMC20003220
(117140), SMINT10000420 (601615), SMINT10000570 (604814), SMINT10001000 (603851), SMINT10001030
(605759), SMINT20004000 (601278), SPLEN10001430 (163905), SPLEN20001970 (601940), STOMA20000880
(147220),
STOMA20003960 (300111), SYNOV20013740 (604076), SYNOV20014510 (600661), SYNOV20016480 (131222),
50 603041), TEST10001270 (601313;173900), TESTH10001310 (186982), TESTI20001200 (194510), TESTI20001770
(146650), TESTI20002530 (605440), TESTI20006000 (179838), TESTI20006990 (602591), TESTI20007820
(126650,214700), TESTI20008830 (160794), TESTI20011800 (190370), TESTI20012690 (109720), TESTI20015120
(604700), TESTI20018520 (602346), TESTI20018790 (300024), TESTI20021490 (604073), TESTI20025160
(300097),
55 TESTI20027070 (173335), TESTI20027290 (300127), TESTI20029120 (600855), TESTI20033250 (168730),
TESTI20049820 (176894), TESTI20053960 (604074), TESTI20068660 (603395), TESTI20071830 (605769),
TESTI20074640 (603899), TESTI20079510 (116930), TESTI20086570 (300153), TESTI20140360 (170100),
THYMU10000830 (600857), THYMU10001760 (116930), THYMU10003590 (602857), THYMU10004910 (604908),

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TRACH20002370 (602277), UTERU10000960 (603931), UTERU20000470 (602070)

[0230] The clones predicted to belong to the category of enzyme and/or metabolism-related protein are the following 168 clones.

3NB692002810, ADRGL10001600, ADRGL10001650, BGGI120005330, BNGH410000340, BNGH410001770,
5 BRACE10000420, BRACE20015080, BRACE20022020, BRACE20024680, BRACE20026850, BRACE20027360,
BRACE20027720, BRACE20027920, BRACE20071380, BRACE20084430, BRAWH20001770, BRAWH20006510,
BRAWH20006860, BRAWH20009840, BRAWH20011660, BRAWH20014180, BRAWH20014840, BRAWH20036890,
BRAWH20059980, BRAWH20069890, BRAWH20089560, CTONG20013660, CTONG20019110, DFNES20002120,
FCBBF20007330, FCBBF20015380, FEBRA20000350, FEBRA20001290, FEBRA20003110, FEBRA20024420,
10 FEBRA20041100, FEBRA20045920, FEBRA20050790, FEBRA20052160, FEBRA20062700, FEBRA20063160,
HEART20000350, HHDP20000450, HHDP20000450, HLUNG10001050, HLUNG20002550, HSYRA10001680,
HSYRA20005100, HSYRA20015740, IMR3220008380, IMR3220009190, IMR3220012180, IMR3220013170,
KIDNE20000410, KIDNE20003470, KIDNE20004220, KIDNE20005130, KIDNE20033050, KIDNE20040840,
KIDNE20046810, KIDNE20056290, KIDNE20060530, KIDNE20063760, KIDNE20068800, KIDNE20073280,
15 KIDNE20073520, KIDNE20078100, LIVER10000670, LIVER10002300, MAMGL10001780, MESAN20002910,
MESAN20005010, NT2NE10000730, NT2NE10001850, NT2NE20002140, NT2NE20003270, NT2NE20003690,
NT2NE20005860, NT2NE20013720, NT2NE20016340, NT2NE20016660, NT2R10000480, NT2R100010100,
NT2R120015400, NT2R120020220, NT2R120025300, NT2R120033010, NT2R120036780, NT2R120037510,
NT2R120051500, NT2R120068550, NT2R120073840, NT2R120074980, NT2R120084810, NT2R120087910,
20 NT2RP70004720, NT2RP70006240, NT2RP70011660, NT2RP70026190, NT2RP70062960, NT2RP70072520,
NT2RP70076100, NT2RP70081440, NT2RP70084060, NT2RP70085570, NT2RP70093700, NTOG10001820,
OCBBF20008240, OCBBF20012100, OCBBF20014080, OCBBF20014940, PANCAR100002210, PEBLM20004790,
PLACE50001050, PLACE50001130, PLACE60003790, PLACE60012810, PLACE60018880, PLACE60044540,
PROST20031170, PROST20032320, PROST20033400, PROST20051210, PROST20064500, SKMUS10001290,
25 SKMUS10001770, SKMUS20000740, SKMUS20007240, SKMUS20008630, SKMUS20009330, SKMUS20011290,
SKMUS10001740, SKMUS10003470, SMINT10000160, SPLEN20001340, STOMA10001860, STOMA20001210,
STOMH200044820, SYNVO20016480, TEST110000700, TEST110001380, TEST120001540, TEST120005910,
TEST120012690, TEST120018270, TEST120022560, TEST120027070, TEST120029120, TEST120034190,
TEST120034980, TEST120040000, TEST120042070, TEST120042950, TEST120044710, TEST120049820,
30 TEST120138320, TEST120140360, TEST130000020, THYMU10000830, THYMU10004910, THYMU20003170,
THYMU20003690, TRACH20000150, TRACH20004720, TRACH20004970, TRACH20009260, UTERU10000960

[0231] The clones predicted to belong to the category of cell division and/or cell proliferation-related protein are the following 23 clones.

BGGI120001610, BRACE20027550, BRACE20076850, BRAWH20005030, BRAWH20005220, FEBRA20075660,
35 HCASM20002140, HLUNG10000640, IMR3220009730, NT2NE20003840, NT2R120006850, NT2R120041900,
NT2R120058110, NTOG10002460, NTOG20008780, SKMUS20016340, SKMUS20003220, SPLEN10001430,
TEST110001680, TEST120001840,
TEST120021050, TEST120035120, TEST120057310

[0232] The clones predicted to belong to the category of cytoskeleton-related protein are the following 60 clones.

40 ADRGL10000020, BRACE20006980, BRACE20008850, BRACE20027960, BRACE20074470, BRACE20076630,
BRACE20078820, BRACE20093070, BRAWH20000480, BRAWH20006220, CTONG20019550, CTONG20028160,
CTONG20055530, DFNES20002680, FCBBF200005910, FEBRA20007720, FEBRA200008810, FEBRA20034290,
FEBRA20043290, FEBRA20072000, HEART20004480, HEART20005020, HLUNG10001100, HSYRA20006050,
45 IMR3220007910, KIDNE20040840, KIDNE20052960, NT2R120014090, NT2R120032220, NT2R120058510,
NT2R120090660, NT2RP70000690, NT2RP70004250, NT2RP70028750, NT2RP70042600, NT2RP70049250,
NT2RP70074220, NTOG20000960, OCBBF20011760, OCBBF20015280, PEBLM10000680, PROST10001670,
PROST20033380, TEST110000420, TEST110000510, TEST120003560, TEST120004350, TEST120006000,
TEST120006990, TEST120008490, TEST120008830, TEST120011410, TEST120015110, TEST120016610,
TEST120020570, TEST120024230, TEST120031090, TEST120031170, TEST120039140, TEST120078720

[0233] The clones predicted to belong to the category of nuclear protein and/or RNA synthesis-related protein are the following 59 clones.

3NB692002810, 3NB6920015280, BGGI120005440, BRACE10001150, BRACE20024780, BRACE20027550,
BRAWH20005030, BRAWH20014180, BRAWH20069890, CTONG20024180, FEBRA20001290, FEBRA20075660,
HEART20003090, HLUNG10000640, HSYRA10001680, HSYRA20000510, IMR3220008630, IMR3220012180,
55 MAMGL10001780, NT2NE10001850, NT2NE20002140, NT2NE20003840, NT2NE20016660, NT2NE20054410,
NT2R120002820, NT2R120006850, NT2R120010910, NT2R120025540, NT2R120041900, NT2R120053350,
NT2R120057230, NT2R120060720, NT2R120067030, NT2R120068550, NT2R120078840, NT2R120087490,
NT2RP70004770, NT2RP70013060, NT2RP70076430, NTOG20008780, PEBLM10000340, PLACE50000580,

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PLACE60003790, PROST20001760, PROST20062600, SKMUS200016340, SKNMC20003220, SPLEN10001430, SPLEN20001970, TEST10001680, TEST120002530, TEST120007840, TEST120021050, TEST120029120, TEST120035120, TEST120057310, TRACH20003930, TRACH20012890

[0234] The clones predicted to belong to the category of protein synthesis and/or transport-related protein are the following 24 clones.

BRACE20078680, FEBRA20075510, IMR3220008380, KIDNE20005190, KIDNE20050420, MESAN20002910, NB9N410001350, NT2NE20005360, NT2RI20032050, NT2RI20032220, NT2RP70000760, NT2RP70076430, NT2RP70093940, OCBBF20008240, PLACE50000580, PROST20000530, SKMUS20000740, SKMUS20008630, TEST120007840, TEST120015120, TEST120018690, TEST120078720, THYMU10005580, UMVEN20001330

[0235] The clones predicted to belong to the category of cellular defense-related protein are the following 6 clones. FEBRA20014550, NT2RI20037510, NT2RI20053350, NT2RP70029060, NT2RP70062960, PLACE50001700

[0236] The clones predicted to belong to the category of development and/or differentiation-related protein are the following 19 clones.

BGG120006930, CTONG20028200, FCBBF50002610, FEBRA20014920, FEBRA20017150, FEBRA20060920, MAMGL10001820, NESOP10000870, NHNPC10001240, NT2RI20078790, NT2RP70008120, NT2RP70018560, NT2RP70045410, OCBBF20002770, SALGL10000650, SMINT10001000, TEST10000550, TEST12002670, TEST120078140

[0237] The clones predicted to belong to the category of DNA-binding and/or RNA-binding protein are the following 158 clones.

3NB6920002810, 3NB6920010220, 3NB6920015110, 3NB6920015570, ADRGL10000650, BGG120006840, BGG120006930, BNGH410000800, BNGH420005320, BRACE20014550, BRACE20020910, BRACE20024090, BRACE20024780, BRACE20077140, BRAWH10001640, BRAWH10001680, BRAWH20000340, BRAWH20006330, BRAWH20009010, BRAWH20014180,

BRAWH20069890, CTONG20025580, CTONG20028200, D3OST20001840, FCBBF10005980, FCBBF20009510, FCBBF50002610, FEBRA20003970, FEBRA20004540, FEBRA20008560, FEBRA20009720, FEBRA20017150, FEBRA20017900, FEBRA20050140, FEBRA20064760, FEBRA20067360, FEBRA20069420, FEBRA20072800, HEART20003090,

HLUNG10000760, HSYRA10001370, HSYRA20016310, IMR3210002420, IMR3220007420, IMR3220008630, KIDNE20000510, KIDNE20039940, KIDNE20061490, KIDNE20078110, NESOP10000870, NHNPC10000840, NHNPC10001240, NHNPC20002120, NT2NE20002590, NT2NE20003840, NT2NE20008090, NT2NE20016660, NT2NE20054410, NT2RI20003410,

NT2RI20004210, NT2RI20006850, NT2RI20010830, NT2RI20010910, NT2RI20025410, NT2RI20025850, NT2RI20057230, NT2RI20060710, NT2RI20067350, NT2RI20071330, NT2RI20074390, NT2RI20078790, NT2RI20077880, NT2RI20087140, NT2RI20087490, NT2RI20090650, NT2RP60001000, NT2RP60001270, NT2RP70002710, NT2RP70008120,

NT2RP70013060, NT2RP70018560, NT2RP70024500, NT2RP70032030, NT2RP70042040, NT2RP70045410, NT2RP70046560, NT2RP70055130, NT2RP70061620, NT2RP70062960, NT2RP70064900, NT2RP70069660, NT2RP70075370, NT2RP70081670, NT2RP70085570, NT2RP70087200, NT2RP70090190, NTONG20003340, NTONG20008780, NTONG20015500,

OCBBF20011010, OCBBF20015860, PEBLM10000340, PEBLM20001120, PEBLM20002700, PEBLM20003080, PLACE60002050, PLACE60005550, PLACE60021510, PLACE60030380, PROST20001760, PROST20003250, PROST20018230, PROST20031170, PROST20062600, PROST20073170, SALGL10000650, SKMUS10000640, SKMUS20014920, SKMUS20016340,

SKNMC20000650, SKNMC20002240, SKNMC20003220, SKNMC20003560, SMINT10001000, SMINT20005450, SPLEN10001430, SPLEN20000020, SPLEN20000720, SPLEN20001970, SYNOV20010140, SYNOV20013740, SYNOV20014510, TEST110000550, TEST120001200, TEST120007070, TEST120010490, TEST120013450, TEST12001560, TEST120018150,

TEST120021050, TEST120021490, TEST12002670, TEST120027890, TEST120030710, TEST120033270, TEST120034130, TEST120035120, TEST120053960, TEST120074640, TEST120074860, TEST120078640, THYMU10004590, TRACH20000790, TRACH20002370, TRACH20009440, TRACH20012890, UTERU10001600

[0238] The clones predicted to belong to the category of ATP binding and/or GTP-binding protein are the following 63 clones.

3NB6920002810, BNGH410000390, BRACE20022020, BRACE20028120, BRACE20071380, BRAWH20000480, BRAWH20006860, BRAWH20066220, CTONG20013200, DFNES20002680, FEBRA20043290, FEBRA20052160, FEBRA20072000, FEBRA20075510, HHDP20000550, HLUNG20001160, HSYRA10001680, HSYRA20005100, HSYRA20060500, KIDNE20040840, MAMGL10001780, MESAN20002910, NB9N410001350, NT2NE20003690, NT2NE20005170, NT2NE20016660, NT2NE20055170, NT2RI20068550, NT2RI20073840, NT2RP70004250, NT2RP70011660, NT2RP70029060, NT2RP70036290, NT2RP70042600, NT2RP70046870, NT2RP70062960,

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NT2RP70081370, NT2RP70081440, NT2RP70093700, OCBBF20008240, OCBBF20015280, PEBLM20004790, PLACE60001700, PLACE60003790, PROST20018990, PROST20033400, SKMUS20008630, SMINT10000420, TEST120001540, TEST120003560, TEST120005910, TEST120006950, TEST120006990, TEST120008490, TEST120015110, TEST120016610, TEST120022560, TEST120029120, TEST120034980, TEST120042290, TEST120047120, TEST120049820, TEST120057310

[0239] Among the clones other than the ones shown above, NTONG10001300 is a clone which was predicted to highly possibly belong to the category of secretory protein and/or membrane protein based on the result of domain search by Pfam.

FEBRA20017060, NT2RI20066790, SMINT10000710

[0240] The three clones shown above are clones which were predicted to highly possibly belong to the category of glycoprotein-related protein based on the result of domain search by Pfam.

BRACE20080970, BRACE20092120, BRAWH10001300, FEBRA20019890, KIDNE20031850, KIDNE20060140, MESAN20000920, NB9N410000470, NT2RI20071480, NT2RP70088550, NTONG20016120, OCBBF10000910, PROST20094830, SKNSH10003010, SPLEN20002670, TEST120031960, TEST120036250, TEST120037810, TEST120083870, TEST120177400

[0241] The 21 clones shown above are clones which were predicted to highly possibly belong to the category of signal transduction-related protein based on the result of domain search by Pfam.

3NB6920009120, 3NB6920014710, BRACE10001660, BRACE20083850, BRAWH20004760, BRAWH20012030, CTONG20011390, CTONG20018200, FEBRA20007870, FEBRA20043250, HHDP20003150, NT2RI10000270, NT2RI20036950, NT2RI20053680, NT2RI20072540, NT2RI20083360, NT2RP70030550, OCBBF20013070, OCBBF20015270, PLACE60046630, PROST10003430, PROST20067370, SKMUS10001040, SKNMC20015960, TEST120030050, TEST120033540, TEST120035890, TEST120068720, TRACH20004110

[0242] The 29 clones shown above are clones which were predicted to highly possibly belong to the category of transcription-related protein based on the result of domain search by Pfam.

BNGH410001900, BRACE20080970, BRACE20092120, BRAWH20093600, FEBRA20003770, FEBRA20024290, HLUNG10000990, KIDNE20004030, MESAN20000920, NB9N420001040, NT2NE10000140, NT2NE20001740, NT2RI20050610, NT2RI20055640, NT2RI20072540, NT2RI20074690, NT2RP70030550, NT2RP70036470, NT2RP70036800, NT2RP70072210, NT2RP70074060, NT2RP70084870, NTONG10001300, NTONG10002640, NTONG20016120, OCBBF10000910, OCBBF10001190, OCBBF20007190, SKMUS20001170, SKMUS200016620, SKNMC20000970, SKNMC20015960, SYNOV10001280, TEST120002380, TEST120006270, TEST120013300, TEST120031520, TEST120036250, TEST120037810, TEST120064830, TEST120083870, TRACH20006750, TRACH20016070

[0243] The 43 clones shown above are clones which were predicted to highly possibly belong to the category of enzyme and/or metabolism-related protein based on the result of domain search by Pfam.

NT2RI20064120

[0244] The clone shown above is a clone which was predicted to highly possibly belong to the category of cell division and/or cell proliferation-related protein based on the result of domain search by Pfam.

BRACE20083800, KIDNE20004970

[0245] The two clones shown above are clones which were predicted to highly possibly belong to the category of cytoskeleton-related protein based on the result of domain search by Pfam.

3NB6920009120, 3NB6920014710, BRACE10001660, BRACE20083850, BRAWH20004760, BRAWH20012030, BRAWH20064500, CTONG20011390, CTONG20018200, FEBRA20007870, FEBRA20043250, HCASM20003070, HHDP20003150, NT2RI10000270, NT2RI20036950, NT2RI20072540, NT2RI20083360, NT2RP70012310, NT2RP70030550, NT2RP70036470, OCBBF20013070, OCBBF20015270, PLACE60046630, PROST10003430, PROST20067370, SKMUS10001040, SKNMC20000970, SKNMC20015960, TEST120030050, TEST120032280, TEST120033540, TEST120035890, TEST120068720, TRACH20004110

[0246] The 34 clones shown above are clones which were predicted to highly possibly belong to the category of DNA-binding and/or RNA-binding protein based on the result of domain search by Pfam.

NT2RI20064120

[0247] The clone shown above is a clone which was predicted to highly possibly belong to the category of ATP-binding and/or GTP-binding protein based on the result of domain search by Pfam.

[0248] The 178 clones shown below are clones which were unassignable to any of the above-mentioned categories, but have been predicted to have some functions based on homology search for their full-length nucleotide sequences and motif search in their deduced ORFs. Clone Name, Definition in the result of homology search or Motif Name in the motif search, demarcated by a double slash mark (/), are shown below.

3NB6910001160/STEROIDOGENIC ACUTE REGULATORY PROTEIN PRECURSOR.

3NB6910001290/KRAB box

3NB6910001730/R101/ZK632.3/MJ0444 family

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- 3NB6920014330//Domain of unknown function
ASTR020000950//SNAP-25 family
BNGH410000030//R. norvegicus trg mRNA.
BNGH410000290//SPRY domain
- 5 BRACE20005250//DRR1 PROTEIN (TU3A PROTEIN).
BRACE20005650//ATP synthase ab C terminal
BRACE20013750//Hepatitis C virus non-structural protein NS4a
BRACE20014770//HUNTINGTIN ASSOCIATED PROTEIN 1 (HAP1).
BRACE20016730//Mus musculus mdgl-1 mRNA, complete cds.
- 10 BRACE20017370//P.vivax pval gene.
BRACE20019440//Protein of unknown function DUF82
BRACE2DD2431D//P53-INDUCED PROTEIN 11.
BRACE20028960//Mus musculus mRNA for Ca2+ dependent activator protein for secretion, complete cds.
BRACE20077840//Putative Protein that mediates attachment of autophagosomes to microtubules, by similarity to yeast
15 aut2 [Schizosaccharomyces pombe].
BRACE20093610//Bacterial type II secretion system protein
BRAWH20003230//Proline rich protein
BRAWH20009440//Arabidopsis thaliana pollenless3 (178) gene, complete cds;
beta-9 tubulin (TUB9) gene, partial cds; and unknown gene.
- 20 BRAWH20014610//TS-N domain/ UBA domain
BRAWH20080440//PPR repeat
BRAWH20076050//LORICRIN.
CTONG20027210//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13.
CTONG20028030//Domain of unknown function DUF19// Ribosomal protein S18
- 25 CTONG20064490//Drosophila melanogaster 26S proteasome regulatory complex subunit p42A mRNA, complete cds.
DFNES20004320//Homo sapiens ubiquitous TPR-motif protein Y isoform (UTY) gene, partial cds; alternatively spliced.
FCBBF10006870//Mus musculus Rap2 interacting protein 8 (RPIP8) mRNA, complete cds.
FCBBF20002320//T-box
FCBBF20002760//ALPHA SCRUIIN.
- 30 FCBBF20012110//Leishmania major partial ppg1 gene for proteophosphoglycan.
FCBBF20016720//Domain of unknown function DUF94
FEBRA20000530//Drosophila melanogaster Diablo (dho) mRNA, complete cds.
FEBRA20005360//Homo sapiens paraneoplastic cancer-testis-brain antigen (MA5) mRNA, complete cds.
FEBRA20007570//Homo sapiens BM-009 mRNA, complete cds.
- 35 FEBRA20011330//26S PROTEASOME REGULATORY SUBUNIT S3 (PROTEASOME SUBUNIT P58).
FEBRA20030540//Halocynthia roretzi mRNA for HrPET-1, complete cds.
FEBRA20044900//R. norvegicus mRNA for CPG2 protein.
FEBRA20048180//DRR1 PROTEIN (TU3A PROTEIN).
FEBRA20053800//Homo sapiens ubiquitous TPR-motif protein Y isoform (UTY) gene, partial cds; alternatively spliced.
- 40 FEBRA20057260//TBC domain
FEBRA20068730//Trg protein
HCASM10000210//Plasmodium berghei strain NYU2 merozoite surface protein-1 mRNA, partial cds.
HCASM20005360//Macrophage migration inhibitory factor
HEART20004110//POT family
- 45 HEART20005680//Nerve growth factor family
HHDPC20001150//Mus musculus putative secreted protein ZSIG37 (Zsig37) mRNA, complete cds.
HHDPC20001490//Mus musculus partial mRNA for muscle protein 534 (mg534 gene). HHDPC20004560//2S seed
storage family
HHDPC20004620//FAD binding domain
- 50 HSYRA10001190//PROBABLE GYP7 PROTEIN (FRAGMENT).
HSYRA10001780//Alpha-2-macroglobulin family N-terminal region
HSYRA20001350//CELL POLARITY PROTEIN TEA1.
HSYRA20014780//Von Willebrand factor type A domain
HSYRA20016210//HesB-like domain
- 55 IMR3220002230//HINT PROTEIN (PROTEIN KINASE C INHIBITOR 1) (PKCI-1) (17 KD (NHIBITOR OF PROTEIN
KINASE C).
IMR3220014910//Rattus norvegicus tricarboxylate carrier-like protein mRNA, complete cds.
KIDNE10001520//Mus musculus yolk sac permease-like molecule 1 (YSPL-1) mRNA, complete cds.

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- KIDNE20003750//Mus musculus mRNA for granuphilin-a, complete cds.
 KIDNE20005740//Staphylococcus epidermidis putative cell-surface adhesin SdrF (sdrF) gene, complete cds.
 KIDNE20043440//Vacuolar protein sorting-associated protein - fission yeast
 KIDNE20056760//NEURONAL PROTEIN.
 5 KIDNE20060300//Gallus gallus syndesmos mRNA, complete cds.
 KIDNE20062480//Scorpion short toxins
 KIDNE20067750//Homo sapiens PTOV1 (PTOV1) gene, complete cds.
 LIVER10000790//Rattus norvegicus fertility related protein WMP1 mRNA, complete cds.
 MAMGL10000560//K-box region
 10 MESAN10001010//Rat trg gene product
 NB9N420004950//PROBABLE NUCLEAR ANTIGEN.
 NT2NE10000180//SUPPRESSOR PROTEIN SRP40.
 NT2NE10000630//Gallus gallus Dach2 protein (Dach2) mRNA, complete cds.
 NT2NE20007630//Matrix protein (MA), p15
 15 NT2NE20013370//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.
 NT2NE20016970//MSF1 PROTEIN.
 NT2NE20035690//Homo sapiens phosphoinositol 3-phosphate-binding protein-2 (PEPP2) mRNA, complete cds.
 NT2NE20053710//Ank repeat
 NT2RI20006690//TRICHOHYALIN.
 20 NT2RI20013420//Mus musculus cyclin ania-5b mRNA, partial cds.
 NT2RI20013850//Homo sapiens P381P (P381P) mRNA, complete cds.
 NT2RI20015190//Homo sapiens misato mRNA, partial cds.
 NT2RI20016210//Probable transposase - human transposon MER37
 NT2RI20022700//X123 protein
 25 NT2RI20025170//Homo sapiens PAR3 (PAR3) mRNA, complete cds.
 NT2RI20029260//ARP2/3 COMPLEX 16 KDA SUBUNIT (P16-ARC).
 NT2RI20029700//EF hand// EF hand
 NT2RI20043040//Homo sapiens NY-REN-2 antigen mRNA, complete cds.
 NT2RI20046060//K+ channel tetramerisation domain
 30 NT2RI20061830//Proline-rich protein M14 precursor
 NT2RI20065060//Drosophila melanogaster rudimentary gene, intron 3; anon-15AB gene, complete cds.
 NT2RI20077230//Homo sapiens BR13 mRNA, complete cds.
 NT2RI20082210//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).
 NT2RI20088120//AXONEME-ASSOCIATED PROTEIN MST101(2).
 35 NT2RI20091440//SPRY domain
 NT2RP60000080//Homo sapiens Pig11 (PIG11) mRNA, complete cds.
 NT2RP60000720//Pinus taeda clone PtaAGP6 putative arabinogalactan protein mRNA, complete cds.
 NT2RP70009060//Medicago truncatula mRNA for 85p protein (85p gene).
 NT2RP70010800//Mus musculus mRNA for MILI (Miwi like), complete cds.
 40 NT2RP70022430//Tax1-binding protein TRX - human.
 NT2RP70028290//Scm-related gene containing four mbt domains [Mus musculus].
 NT2RP70033040//YceA protein homolog ybfQ - Bacillus subtilis.
 NT2RP70036320//Microfilarial sheath protein
 NT2RP70039600//Calpain inhibitor repeat
 45 NT2RP70042330//HYPOTHETICAL PROTEIN MJ0941.
 NT2RP70049150//Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, complete cds.
 NT2RP70052050//Human transformation-related protein mRNA, 3' end.
 NT2RP70084410//Polybromo 1 protein - chicken
 NTONG10000520//Rattus norvegicus mRNA for Kelch related protein 1 (krp1 gene).
 50 NTONG10001230//Mus msuculus mRNA, partial cds, clone CLFEST42.
 OCBBF10001220//RING CANAL PROTEIN (KELCH PROTEIN).
 OCBBF20010750//Spectrin repeat
 OCBBF20011400//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS8.
 OCBBF20014020//Mus musculus NSD1 protein mRNA, complete cds.
 55 PEBLM10001440//Trg
 PEBLM20002130//Mus musculus genes for integrin aM290, hapsin, partial and complete cds.
 PLACE50000370//Homo sapiens mRNA for hVPS11, complete cds.
 PLACE60004290//Gag P30 core shell protein

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- PLACE60021020//Integrase Zinc binding domain// Integrase Zinc binding domain// DnaJ central domain (4 repeats)
PLACE60024190//TRICHOHYALIN.
PLACE60032040//Hirudin
PLACE60033990//SP1 DROIN 1 (DRAGLINE SILK FIBROIN 1) (FRAGMENT).
5 PLACE60038500//Homo sapiens mitochondrial solute carrier mRNA, complete cds.
PLACE60043970//Takifugu rubripes retinitis pigmentosa GTPase regulator-like protein gene, partial cds.
PLACE60044640//Human placenta (Dill48) mRNA, complete cds.
PROST20023380//Coc3 protein
PROST20034720//IMMEDIATE-EARLY PROTEIN.
10 PROST20079740//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) (FRAGMENT).
SALGL10000050//Permeases for cytosine/purines, uracil, thiamine, allantoin
SALGL10000470//NG36 [Homo sapiens]
SKMUS20002710//Hepatitis C virus capsid protein
SKMUS20003650//Human (p23) mRNA, complete cds.
15 SKMUS20004580//Mus musculus N-RAP mRNA, complete cds.
SKMUS20009020//BR01 PROTEIN.
SKMUS20009540//Homo sapiens F-box protein Fbx25 (FBX25) mRNA, partial cds.
SKMUS20010080//Mus musculus mRNA for a skeletal muscle and cardiac protein.
SKMUS20011470//Mus musculus RP42 mRNA, complete cds.
20 SKMUS20013640//Laminin EGF-like (Domains III and V)
SKMUS20015430//Homo sapiens HDCMC29P mRNA, partial cds.
SKNMC20010570//F-box domain.
SMINT20001450//Halocynthia roretzi mRNA for HrPET-3, complete cds.
SMINT20002270//Disintegrin/ Trans-activation protein X
25 SMINT20003960//A kinase anchor protein AKAP-KL isoform 2
STOMA20002890//Adaptin N terminal region
SYNOV20002910//Arabinogalactan-like protein
SYNOV20008200//Trichoplusia ni transposon IFP2.
TEST110000250//M. musculus mRNA for testis-specific protein, DDC8.
30 TEST110000640//Fugu rubripes sex comb on midleg-like 2 protein (SCML2) gene, complete cds.
TEST110001910//Homo sapiens 88-kDa Golgi protein (GM88) mRNA, complete cds.
TEST120000440//TRICHOHYALIN.
TEST120002070//NIFU-LIKE PROTEIN.
TEST120002080//Homo sapiens mRNA for Gab2, complete cds.
35 TEST120014120//TRICHOHYALIN.
TEST120016650//IMMEDIATE-EARLY PROTEIN.
TEST120022230//Chlamydomonas reinhardtii strain 1132D- flagellar
protofilament ribbon protein (RIB43a) mRNA, complete cds.
TEST120022940//MOB2 PROTEIN (MPS1 BINDER 2).
40 TEST120024610//TRICHOHYALIN.
TEST120030590//TESTIS-SPECIFIC PROTEIN PBS13.
TEST120030740//TRICHOHYALIN.
TEST120031300//TPR Domain
TEST120033560//F-box domain.
45 TEST120035510//Proliferating-cell nucleolar antigen P120-like protein - Archaeoglobus fulgidus.
TEST120035740//A-KINASE ANCHOR PROTEIN 150 (AKAP 150) (CAMP-DEPENDENT PROTEIN KINASE REGU-
LATORY SUBUNIT II HIGH AFFINITY BINDING PROTEIN) (P150) (FRAGMENT).
TEST120038940//IQ calmodulin-binding motif// IQ calmodulin-binding motif// IQ calmodulin-binding motif
TEST120040310//Protein of unknown function DUF84
50 TEST120041220//Babesia bigemina 200 kDa antigen p200 mRNA, partial cds.
TEST120052680//Rattus norvegicus RSD-6 mRNA, complete cds.
TEST120054080//SER/THR-RICH PROTEIN T10 IN DGCR REGION.
TEST120065720//PROTEIN D52 (N8 PROTEIN).
TEST120078670//RING CANAL PROTEIN (KELCH PROTEIN).
55 TEST120080330//Ribosomal protein L14pL23e
TEST120083430//TPR Domain
THYMU10000020//Homo sapiens mRNA for Golgi protein (GPP34 gene).
THYMU10002910//Homo sapiens AP-4 adaptor complex beta4 subunit mRNA, complete cds.

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THYMU20002380//Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)

TRACH10000300//Anabaena PCC7120 hetC gene, complete cds.

TRACH20007800//Homo sapiens PTH-responsive osteosarcoma B1 protein (B1) mRNA, complete cds.

TRACH20008940//Protein TSG24 (MEIOTIC CHECK POINT REGULATOR).

5 TRACH20013950//Homo sapiens NY-REN-25 antigen mRNA, partial cds.

UMVEN10001220//Corticotropin-releasing factor family

[0249] With respect to the remaining 476 clones, there are so far no information available for estimating their functions. However, there is the possibility that the functions of these clones will be revealed in future. Their Clone Names are indicated below.

10 3NB6920013490, 3NB6920016370, 3NB6920017190, ADRGL10001820, ADRGL20004280, ASTRO20004800, BGGI110002850, BNGH410000130, BNGH410000170, BNGH410000150, BNGH420004740, BRACE10000200, BRACE10000070, BRACE10001590, BRACE20000770, BRACE20001000, BRACE20001410, BRACE20003320, BRACE20004210, BRACE20005050, BRACE20005450, BRACE20009880, BRACE20010700, BRACE20011880, BRACE20013740, BRACE20015430, BRACE20016920, BRACE20018650, BRACE20018980, BRACE20020500, BRACE20021510, BRACE20021760, BRACE20024950, BRACE20025900, BRACE20027520, BRACE20028800, BRACE20028610, BRACE20032850, BRACE20033190, BRACE20033980, BRACE20034310, BRACE20035160, BRACE20035270, BRACE20035390, BRACE20035940, BRACE20071530, BRACE20072010, BRACE20072320, BRACE20075270, BRACE20075630, BRACE20076370, BRACE20076460, BRACE20077080, BRACE20077270, BRACE20077670, BRACE20077680, BRACE20079020, BRACE20081140, BRACE20084800, BRACE20084880, BRACE20086530, BRACE20087080, BRACE20087540, BRACE20088570, BRACE20089990, BRACE20090140, BRACE20092740, BRACE20092750, BRACE20093110, BRACE20094370, BRACE20095170, BRAWH10000070, BRAWH10001740, BRAWH20000930, BRAWH20002480, BRAWH20005540, BRAWH20008660, BRAWH20008920, BRAWH20011030, BRAWH20047310, BRAWH20064930, BRAWH20069600, BRAWH20074060, BRAWH20089030, BRAWH20092270, BRAWH20094860, CTONG200003030, CTONG20007710, CTONG20008270, CTONG20020730, CTONG20021430, CTONG20024530, CTONG20029650, DFNES20002920, FCBBF10006860, FCBBF10006910, FCBBF10007320, FCBBF10007600, FCBBF20001050, FCBBF20001950, FCBBF20005760, FCBBF20006770, FCBBF20008080, FCBBF20012990, FCBBF20014800, FCBBF20017180, FCBBF20017200, FEBRA20003300, FEBRA20003910, FEBRA20006800, FEBRA20007400, FEBRA20007710, FEBRA20008740, FEBRA20009010, FEBRA20009590, FEBRA20011970, FEBRA20015900, FEBRA20021940, FEBRA20027270, FEBRA20027830, FEBRA20028820, FEBRA20028970, FEBRA20029080, FEBRA20033080, FEBRA20042240, FEBRA20042370, FEBRA20042930, FEBRA20044120, FEBRA20044430, FEBRA20053770, FEBRA20054270, FEBRA20057520, FEBRA20059980, FEBRA20061500, FEBRA20063540, FEBRA20066270, FEBRA20074140, FEBRA20074580, FEBRA20076220, HCASM10001150, HCASM20005340, HLUNG10000300, HLUNG20003140, HLUNG20004800, HLUNG20005010, HSYRA10001480, HSYRA20002480, HSYRA20002530, HSYRA20007600, HSYRA20011530, IMR3210000740, IMR3210000750, IMR3210001650, IMR3220006090, IMR3220009350, IMR3220009530, IMR3220011850, IMR3220016000, IMR3220017240, KIDNE10000280, KIDNE10000500, KIDNE10001450, KIDNE20001920, KIDNE20002440, KIDNE20002450, KIDNE20002660, KIDNE20033350, KIDNE20033770, KIDNE20037520, KIDNE20040340, KIDNE20040540, KIDNE20042940, KIDNE20045200, KIDNE20045340, KIDNE20045790, KIDNE20048840, KIDNE20048790, KIDNE20059370, KIDNE20070050, KIDNE20070770, KIDNE20073560, LIVER10000990, LIVER10002780, LIVER10003030, LIVER20004460, LIVER20005150, MAMGL10000350, MESAN20002670, MESAN20003370, NBN410001210, NBN410001450, NHPNC10001010, NT2NE10000040, NT2NE10001200, NT2NE20000380, NT2NE20000560, NT2NE20000640, NT2NE20006360, NT2NE20007060, NT2NE20007870, NT2NE20008020, NT2NE20009800, NT2NE20011560, NT2NE20013240, NT2NE20013840, NT2NE20014030, NT2NE20014280, NT2NE20015300, NT2NE20016230, NT2NE20016480, NT2NE20004490, NT2RI10000160, NT2RI10001640, NT2RI20000540, NT2RI20002700, NT2RI20002940, NT2RI20006710, NT2RI20007380, NT2RI20008850, NT2RI20012350, NT2RI20012440, NT2RI20014100, NT2RI20017260, NT2RI20026540, NT2RI20028020, NT2RI20028520, NT2RI20030190, NT2RI20030670, NT2RI20033040, NT2RI20033380, NT2RI20035560, NT2RI20040590, NT2RI20043980, NT2RI20047830, NT2RI20048400, NT2RI20049160, NT2RI20049840, NT2RI20056280, NT2RI20061270, NT2RI20063450, NT2RI20064870, NT2RI20065530, NT2RI20066670,

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NT2RI20067880, NT2RI20071160, NT2RI20072140, NT2RI20073860, NT2RI20075070, NT2RI20075720,
 NT2RI20075890, NT2RI20077290, NT2RI20077510, NT2RI20085260, NT2RI20085650, NT2RI20088010,
 NT2RI20090830, NT2RP60000170,
 NT2RP60000590, NT2RP70000410, NT2RP70003910, NT2RP70005790, NT2RP70013350, NT2RP70024490,
 5 NT2RP70025540, NT2RP70028410, NT2RP70030500, NT2RP70030910, NT2RP70047510, NT2RP70047660,
 NT2RP70049750, NT2RP70052190, NT2RP70054680, NT2RP70054930, NT2RP70063740, NT2RP70066210,
 NT2RP70067010, NT2RP70069800,
 NT2RP70071140, NT2RP70073590, NT2RP70079300, NT2RP70081420, NT2RP70086230, NT2RP70092150,
 NT2RP70092590, NT2RP70093630, NT2RP70093970, NT2RP70094660, NT2RP70095020, NTONG10000330,
 10 NTONG20005830, NTONG20009850, NTONG20011370, NTONG20014280, OCBBF10000670, OCBBF10000860,
 OCBBF10001040, OCBBF20000130,
 OCBBF20001260, OCBBF20002870, OCBBF20009040, OCBBF20017080, PANCR10001850, PEBLM10000290,
 PEBLM10001800, PEBLM20000300, PEBLM20001260, PEBLM20001470, PLACE60001530, PLACE60000440,
 PLACE60000700, PLACE60000800, PLACE60001370, PLACE60002630, PLACE60003710, PLACE60004240,
 15 PLACE60005230, PLACE60005500,
 PLACE60009530, PLACE60012940, PLACE60019230, PLACE60019250, PLACE60026920, PLACE60029490,
 PLACE60030940, PLACE60031090, PLACE60033720, PLACE60037400, PLACE60040050, PLACE60043120,
 PLACE60043360, PLACE60044910, PLACE60046870, PLACE60049310, PROST10001520, PROST10002460,
 PROST10005640, PROST20002060,
 20 PROST20002670, PROST20002740, PROST20004630, PROST20017390, PROST20017960, PROST20019980,
 PROST20021620, PROST20025910, PROST20028420, PROST20031020, PROST20032100, PROST20033030,
 PROST20037320, PROST20044810, PROST20056040, PROST20061960, PUAE10000810, SKMUS10001240,
 SKMUS20003430, SKMUS20004670,
 SKMUS20004680, SKMUS20008470, SKMUS20009450, SKMUS20015010, SKMUS20016080, SKMUS20016310,
 25 SKMUS20016710, SKNMC10000100, SKNMC10000100, SKNMC10001100, SKNMC10001590, SKNMC10001680,
 SKNMC10002640, SKNMC20003050, SKNMC20005930, SKNMC20006120, SKNMC20015550, SKNSH10000860,
 SKNSH10003080, SKNSH20001510,
 SKNSH20001630, SMINT10000390, SMINT10000540, SMINT20000400, SMINT20002390, SMINT20005580,
 SPLEN10000490, SPLEN20000370, SPLEN20002420, SPLEN20004430, SPLEN20005410, STOMA10000470,
 30 STOMA10001330, STOMA20001880, STOMA20004780, SYNOV10001640, SYNOV20011440, SYNOV20014570,
 TEST110000230, TEST110001250,
 TEST110001630, TEST110001790, TEST120000180, TEST120001790, TEST120003720, TEST120004620,
 TEST120005200, TEST120006710, TEST120008190, TEST120008300, TEST120009510, TEST120010080,
 TEST120010820, TEST120013060, TEST120015930, TEST120017580, TEST120017660, TEST120017920,
 35 TEST120018260, TEST120018290,
 TEST120018980, TEST120019500, TEST120019680, TEST120019910, TEST120020480, TEST120020900,
 TEST120022450, TEST120022640, TEST120023610, TEST120023690, TEST120024150, TEST120025440,
 TEST120028060, TEST120028400, TEST120029650, TEST120032560, TEST120032800, TEST120032990,
 TEST120033780, TEST120034180,
 40 TEST120035410, TEST120035800, TEST120037270, TEST120041110, TEST120042430, TEST120049290,
 TEST120051550, TEST120054920, TEST120062380, TEST120062550, TEST120064250, TEST120069790,
 TEST120073580, TEST120074020, TEST120076130, TEST120077500, TEST120081390, TEST120082340,
 TEST120082400, TEST120084400,
 THYMU10000320, THYMU10001050, THYMU10003660, THYMU10004790, THYMU10005270, THYMU20001400,
 45 TRACH10000180, TRACH10000570, TRACH10001060, TRACH20002350, TRACH20004610, TRACH20011920,
 TRACH20014000, UTERU200003380, UTERU20005410, UTERU20005690

EXAMPLE 7

Expression frequency analysis *in silico*

[0250] The cDNA libraries derived from various tissues and cells as indicated in Example 1 were prepared, and cDNA clones were selected from each library at random. The 5'-end sequences were determined and the database was constructed based on the data. The database was constructed based on the nucleotide sequences of 770,546 clones, and thus the population of the database is large enough for the analysis.

[0251] Then, clones having a homologous sequence are categorized into a single cluster (clustering) by searching the nucleotide sequences of respective clones in this database with the program of nucleotide sequence homology search; the number of clones belonging to each cluster was determined and normalized for every library; thus, the

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ratio of a certain gene in each cDNA library was determined. This analysis gave the information of the expression frequency of genes in tissues and cells which were sources of the cDNA libraries.

[0252] Then, in order to analyze the expression of a gene containing the nucleotide sequence of the cDNA of the present invention in tissues and cells, the library derived from a tissue or a cell used in the large-scale cDNA analysis was subjected to the comparison of the expression levels between tissues or cells. Namely, the expression frequency was analyzed by comparing the previously normalized values between tissues and/or cells for which the nucleotide sequences of 600 or more cDNA clones had been analyzed. By this analysis, some of the genes were revealed to be involved in the pathology and functions indicated below. Each value in Tables 3 to 39 shown below represents a relative expression frequency; the higher the value, the higher the expression level.

Osteoporosis-related genes

[0253] Osteoporosis is a pathology in which bones are easily broken owing to overall decrease in components of bone. The onset involves the balance between the functions of osteoblast producing bone and osteoclast absorbing bone, namely bone metabolism. Thus, the genes involved in the increase of osteoclasts differentiating from precursor cells of monocyte/macrophage line (Molecular Medicine 38, 642-648, (2001)) are genes involved in bone metabolism associated with osteoporosis.

[0254] A nucleotide sequence information-based analysis was carried out to identify the genes whose expression frequencies are higher or lower in CD34+ cell (cell expressing a glycoprotein CD34) treated with the osteoclast differentiation factor (Molecular Medicine 38, 642-648, (2001)) than in the untreated CD34+ cell, which is the precursor cell of monocyte/macrophage line. The result of comparative analysis for the frequency between the two cDNA libraries prepared from the RNA of CD34+ cells (CD34C) and from the RNA of CD34+ cells treated with the osteoclast differentiation factor (D3OST, D60ST or D90ST) showed that the genes whose expression levels were different between the two were the following clones (Table 3).

KIDNE20062480, NT2RI20016570, PLACE60020840, 3NB6920002810, BRACE20035270, BRAWH20000340, FEBRA20062700, HSYRA20011030, NT2RP70030910, OCBBF20011240, PLACE60043120, SYNNOV20011440, HCASM10001150, IMR3220016000, NT2RI20082210, D3OST20001840, FEBRA20012940, FEBRA20021910, IMR3220002230, IMR3220012180, NT2RI20000640, NT2RI20010910, NT2RI20058110, NT2RP60000350, NT2RP70011660, PEBLM20003950, PLACE60049310, PROST20062600, TESTI20007840, TESTI20040310, TESTI20080200, THYMU10003590, TRACH10000630, TRACH20007800, CD34C20000510, HSYRA20016210, KIDNE20004030, KIDNE20073280, NT2RP70055020, PLACE60043960, SKMUS10000220

[0255] These genes are involved in osteoporosis.

Genes involved in neural cell differentiation

[0256] Genes involved in neural cell differentiation are useful for treating neurological diseases. Genes with varying expression levels in response to induction of cellular differentiation in neural cells are thought to be involved in neurological diseases.

[0257] A survey was performed for genes whose expression levels are varied in response to induction of differentiation (stimulation by retinoic acid (RA) or growth inhibitor treatment after RA stimulation) in cultured cells of a neural strain, NT2. The result of comparative analysis of cDNA libraries derived from undifferentiated NT2 cells (NT2RM) and the cells subjected to the differentiation treatment (NT2RP, NT2RI or NT2NE) showed that the genes whose expression levels were different between the two were the following clones (Table 4).

SKNMC20000970, 3NB6920009120, BRAWH20006970, KIDNE20062480, NHNPC20002060, NT2NE20053710, NT2RI20000640, NT2RI20004210, NT2RI20006710, NT2RI20009740, NT2RI20013420, NT2RI20013850, NT2RI20014100, NT2RI20025410, NT2RI20033040, NT2RI20035560, NT2RI20036960, NT2RI20051500, NT2RI20053350, NT2RI20057230, NT2RI20071330, NT2RI20075720, NT2RI20083960, NT2RI20087910, NT2RI20090650, NT2RI20094060, NT2RP60000350, NT2RP70000760, NT2RP70036800, NT2RP70071770, NT2RP70074220, TESTI20007840, TESTI20080200, 3NB6920002810, 3NB6920005450, HSYRA20015740, HSYRA20016210, IMR3220016000, KIDNE20060140, NT2RI20014490, NT2RI20015950, NT2RI20022520, NT2RI20025170, NT2RI20025540, NT2RI20030510, NT2RI20040590, NT2RI20040600, NT2RI20053680, NT2RI20058510, NT2RI20066820, NT2RI20067030, NT2RI20074980, NT2RI20075890, NT2RI20078840, NT2RI20084810, NT2RI20089420, NT2RP70002380, NT2RP70023790, NT2RP70029820, NT2RP70049150, NT2RP70055020, NT2RP70065270, NT2RP70069860, NT2RP70075370, NT2RP70079750, NT2RP70092590, OCBBF20000130, PLACE60043970, TESTI20053960, BNGH420004740, HSYRA20002480, NT2NE10000730,

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	NT2NE20000560, NT2NE20003270, NT2NE20008090, NT2NE20014030, NT2RP60000720, NT2RP60001090,
	NT2RP70004770, NT2RP70010800, NT2RP70016660, NT2RP70028750, NT2RP70029060, NT2RP70030550, NT2RP70032030, NT2RP70036320,
	NT2RP70064900, NT2RP70093220, NT2RP70093730, SYN0V20013740, TESTI20021490, TRACH20004720,
5	TRACH20007800, 3NB6920003300, BRACE10000200, BRACE20018550, FEBRA20008740, FEBRA20074580,
	FEBRA20076220, KIDNE20073520, MAMGL10000320, NT2NE20002140, NT2NE20006360, NT2NE20007870, NT2NE20009800, NT2NE20035690,
	NT2RI20002940, NT2RI20014500, NT2RI20016210, NT2RI20029260, NT2RI20037510, NT2RI20055640,
	NT2RI20064120, NT2RI20074390, NT2RI20077230, NT2RI20090660, PLACE60040050, TRACH20012890,
10	3NB6910001730, BRACE10001150, BRACE20011170, BRACE20035270, BRAWH20005220, FEBRA20003970, FEBRA20012450,
	HLUNG20003140, IMR3220009350, IMR3220013170, IMR3220013320, IMR3220014350, NT2NE10000040,
	NT2NE10000140, NT2NE10000180, NT2NE10000230, NT2NE10000630, NT2NE10000830, NT2NE10001200,
	NT2NE10001630, NT2NE10001850, NT2NE20000380, NT2NE20000640, NT2NE20001740, NT2NE20002590, NT2NE20003690,
15	NT2NE20003840, NT2NE20003920, NT2NE20004550, NT2NE20004700, NT2NE20005170, NT2NE20005360,
	NT2NE20005500, NT2NE20005860, NT2NE20006580, NT2NE20007060, NT2NE20007630, NT2NE20008020,
	NT2NE20011560, NT2NE20012470, NT2NE20013240, NT2NE20013370, NT2NE20013640, NT2NE20013720, NT2NE20014280, NT2NE20014350,
20	NT2NE20015300, NT2NE20016230, NT2NE20016260, NT2NE20016340, NT2NE20016480, NT2NE20016660,
	NT2NE20016970, NT2NE20034080, NT2NE20044900, NT2NE20047160, NT2NE20054410, NT2NE20055170,
	NT2NE20057200, OCBBF20009040, OCBBF20015860, PLACE60020840, PROST10005260, SKMUS20008630, SMINT20003960, STOMA20001210,
	SYNOV20001440, TESTI10000230, TESTI20009700, TESTI20040310, THYMU10003290, TRACH20013950,
25	BGGI20010970, BNGH410001980, BRACE10001660, BRACE20014770, BRACE20034490, BRACE20071740,
	BRAWH20009440, BRAWH20036930, CTONG20020730, CTONG20028030, FCBBF10006750, FCBBF20012110, FCBBF20015380, FEBRA20007570,
	FEBRA20043250, FEBRA20068730, HCASM10001150, HCASM20002140, HHDP20000950, HHDP20004620,
	HSYRA10001370, HSYRA10001780, HSYRA20001350, HSYRA20006050, IMR3210001580, IMR3220002230,
30	IMR3220003020, KIDNE20004030, KIDNE20060300, KIDNE20073280, MESAN20005010, NT2RI10000160, NT2RI10000270, NT2RI10000480,
	NT2RI10001640, NT2RI20002700, NT2RI20002820, NT2RI20003410, NT2RI20004120, NT2RI20005970,
	NT2RI20006690, NT2RI20006850, NT2RI20007380, NT2RI20008650, NT2RI20010100, NT2RI20010830,
	NT2RI20010910, NT2RI20012350, NT2RI20012440, NT2RI20014090, NT2RI20015190, NT2RI20015400, NT2RI20016570, NT2RI20017260,
35	NT2RI20018460, NT2RI20018660, NT2RI20020220, NT2RI20020410, NT2RI20021520, NT2RI20022430,
	NT2RI20022700, NT2RI20025300, NT2RI20025850, NT2RI20026540, NT2RI20028020, NT2RI20028520,
	NT2RI20029580, NT2RI20029700, NT2RI20030110, NT2RI20030190, NT2RI20030670, NT2RI20031540, NT2RI20032050, NT2RI20032220,
40	NT2RI20033010, NT2RI20033380, NT2RI20033440, NT2RI20033830, NT2RI20036780, NT2RI20041900,
	NT2RI20042840, NT2RI20043040, NT2RI20043980, NT2RI20044420, NT2RI20047830, NT2RI20048400,
	NT2RI20049160, NT2RI20049840, NT2RI20049850, NT2RI20050610, NT2RI20050870, NT2RI20056280, NT2RI20056470, NT2RI20058110,
	NT2RI20060710, NT2RI20060720, NT2RI20061270, NT2RI20061830, NT2RI20062100, NT2RI20063450,
45	NT2RI20064870, NT2RI20065060, NT2RI20065530, NT2RI20066670, NT2RI20066790, NT2RI20067350,
	NT2RI20067880, NT2RI20068250, NT2RI20068550, NT2RI20070480, NT2RI20070840, NT2RI20070960, NT2RI20071160, NT2RI20071480,
	NT2RI20072140, NT2RI20072540, NT2RI20073030, NT2RI20073840, NT2RI20073860, NT2RI20074690,
	NT2RI20075070, NT2RI20077290, NT2RI20077510, NT2RI20077540, NT2RI20078270, NT2RI20078790,
50	NT2RI20078910, NT2RI20080500, NT2RI20081880, NT2RI20082210, NT2RI20083360, NT2RI20085260, NT2RI20085980, NT2RI20086560,
	NT2RI20087140, NT2RI20087490, NT2RI20088010, NT2RI20088120, NT2RI20089830, NT2RI20091440,
	NT2RI20092150, NT2RI20092890, NTONG10001820, OCBBF20002770, OCBBF20010240, PEBLM10001440,
	PLACE50001130, PLACE60014430, PROST20029600, PUAEN10000570, SALGL10001570, SKMUS10000220, SKMUS20004670, STOMA20002890,
55	SYNOV10001280, TESTI20012690, TESTI20023690, TESTI20028650, TESTI20068720, THYMU10000020,
	THYMU10000830, TRACH20002370, 3NB6910001290, BRACE10000700, BRACE20003320, BRACE20015080,
	BRACE20079020, BRACE20083800,

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BRACE20092740, FEBRA20008810, FEBRA20017150, FEBRA20067930, HHDP20000550, HSYRA20008280, HSYRA20014780, KIDNE10001450, KIDNE20000850, KIDNE20003300, KIDNE20033050, KIDNE20045340, NT2RP60000080, NT2RP60000170, NT2RP60000320, NT2RP60000390, NT2RP60000590, NT2RP60000860, NT2RP60001000,

5 NT2RP60001230, NT2RP60001270, NT2RP70000410, NT2RP70000690, NT2RP70002590, NT2RP70002710, NT2RP70003640, NT2RP70003910, NT2RP70004250, NT2RP70005790, NT2RP70006240, NT2RP70008120, NT2RP70009060, NT2RP70012310, NT2RP70013060, NT2RP70013350, NT2RP70015910, NT2RP70018560, NT2RP70021510, NT2RP70022430,

10 NT2RP70023760, NT2RP70024490, NT2RP70024500, NT2RP70025540, NT2RP70026190, NT2RP70028290, NT2RP70028410, NT2RP70030500, NT2RP70030910, NT2RP70033040, NT2RP70036290, NT2RP70036470, NT2RP70039600, NT2RP70040800, NT2RP70042040, NT2RP70042300, NT2RP70042600, NT2RP70043730, NT2RP70043960, NT2RP70045410,

NT2RP70046560, NT2RP70046870, NT2RP70047510, NT2RP70047660, NT2RP70047900, NT2RP70049250, NT2RP70049750, NT2RP70052050, NT2RP70052190, NT2RP70054680, NT2RP70054330, NT2RP70055130, NT2RP70055200, NT2RP70056120, NT2RP70061880, NT2RP70062960, NT2RP70063040, NT2RP70063740, NT2RP70064080, NT2RP70066210,

NT2RP70067010, NT2RP70068900, NT2RP70071140, NT2RP70071540, NT2RP70072210, NT2RP70072520, NT2RP70073590, NT2RP70073810, NT2RP70074060, NT2RP70075040, NT2RP70076100, NT2RP70076170, NT2RP70076430, NT2RP70079250, NT2RP70079300, NT2RP70081330, NT2RP70081370, NT2RP70081420, NT2RP70081440, NT2RP70081670,

20 NT2RP70083150, NT2RP70084060, NT2RP70084410, NT2RP70084870, NT2RP70085500, NT2RP70085570, NT2RP70086230, NT2RP70087200, NT2RP70088550, NT2RP70090120, NT2RP70090190, NT2RP70091490, NT2RP70091680, NT2RP70092150, NT2RP70092360, NT2RP70093630, NT2RP70093700, NT2RP70093940, NT2RP70093970, NT2RP70094290,

25 NT2RP70094660, NT2RP70094810, NT2RP70094980, NT2RP70095020, NT2RP70095070, NTONG10000980, NTONG10002140, NTONG20002650, NTONG20016120, PEBLM20003950, PROST10005640, PROST20003250, SKNMC20000650, SKNSH10000860, SKNSH20003470, TESTI10000510, TESTI10000960, TESTI20015110, TESTI20074640, TRACH20004610

[0258] These genes are neurological disease-related genes.

Cancer-related genes

[0259] It has been assumed that, distinct from normal tissues, cancer tissues express a distinct set of genes, and thus the expression can contribute to the carcinogenesis in tissues and cells. Thus, the genes whose expression patterns in cancer tissues are different from those in normal tissues are cancer-related genes. Search was carried out for the genes whose expression levels in cancer tissues were different from those in normal tissues.

[0260] The result of comparative analysis of cDNA libraries derived from breast tumor (TBAES) and normal breast (BEAST) showed that the genes whose expression levels were different between the two were the following clones (Table 5).

3N B6910001730, FCBBF10007600, KIDNE20033050, KIDNE20060300, NT2RI20065530, NT2RP60000720, NT2RP70075370, TRACH20004200, LIVER10000670, LIVER10005420, LIVER20000370

[0261] The result of comparative analysis of cDNA libraries derived cervical tumor (TCERX) and normal cervical duct (CERVX) showed that the genes whose expression levels were different between the two were the following clones (Table 6).

BRACE10001590, HHDP20000950, HSYRA20016210, NT2RI20074980, 3NB6920014330, NT2RI20087490, NT2RP60001090, PROST10002200, SKNMC20003220, STOMA20001210

[0262] The result of comparative analysis of cDNA libraries derived from colon tumor (TCOLN) and normal colon (COLON) showed that the genes whose expression levels were different between the two were the following clones (Table 7).

BRACE20028610, BRACE20011170, BRACE20035940, IMR3220013320, NT2NE20053710

[0263] The result of comparative analysis of cDNA libraries derived from esophageal tumor (TESOP) and normal esophagus (NESOP) showed that the genes whose expression levels were different between the two were the following clones (Table 8).

KIDNE20005740, MAMGL10000320, NESOP10000870, NT2RI20056470, NTONG20008000

[0264] The result of comparative analysis of cDNA libraries derived from kidney tumor (TKIDN) and normal kidney (KIDNE) showed that the genes whose expression levels were different between the two were the following clones (Table 9).

3NB6920002810, ADRGL10000020, BNGH420004740, BRACE10000200, BRACE10000420, BRACE10000730,

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BRACE10001590, BRACE20005650, BRACE20016730, BRACE20028120, BRACE20077980, BRACE20083800, BRACE20083850, BRAWH10001740, BRAWH20036930, BRAWH20064500, BRAWH20064930, CTONG20028030, FCBBF20015380, FEBRA20005360, FEBRA20007570, FEBRA20008740, FEBRA20012270, FEBRA20025250, HSYRA20002480, HSYRA20006400, HSYRA20008280, HSYRA20015740, HSYRA20016210, IMR3220009350, LIVER10001110, NT2NE20003920, NT2NE20007630, NT2NE20007870, NT2RI20025410, NT2RI20026540, NT2RI20029580, NT2RI20033380, NT2RI20033830, NT2RI20051500, NT2RI20058110, NT2RI20090650, NT2RP60000720, NT2RP70013350, NT2RP70023790, NT2RP70024490, NT2RP70028750, NT2RP70029060, NT2RP70036800, NT2RP70075370, NT2RP70076100, NTONG10000980, NTONG10002240, NTONG20015500, OCBBF200002310, OCBBF20013070, PEBLM20001470, PEBLM20003950, PLACE60021510, PLACE60040050, PLACE60043970, PROST20051430, STOMA20001210, STOMA20002570, STOMA20002890, SYNOV20011440, TESTI10000230, TESTI20009700, TESTI20021490, TESTI20032800, TESTI20053960, TESTI20080200, TESTI20082400, BGGI120010970, BRACE20004210, BRACE20005250, BRACE20011170, BRACE20020910, BRACE20080970, BRAWH20000340, BRAWH20006970, BRAWH20011680, FCBBF20001950, FEBRA20043250, HLUNG10000640, IMR3220007420, IMR3220014350, KIDNE10000080, KIDNE10000280, KIDNE10000500, KIDNE10001040, KIDNE10001430, KIDNE10001450, KIDNE10001520, KIDNE20000410, KIDNE20000510, KIDNE20000700, KIDNE20000850, KIDNE20001670, KIDNE20001920, KIDNE20002440, KIDNE20002450, KIDNE20002660, KIDNE20003150, KIDNE20003300, KIDNE20003490, KIDNE20003750, KIDNE20004030, KIDNE20004220, KIDNE20004970, KIDNE20005130, KIDNE20005170, KIDNE20005190, KIDNE20005470, KIDNE20031850, KIDNE20033050, KIDNE20033350, KIDNE20033570, KIDNE20033730, KIDNE20033770, KIDNE20037520, KIDNE20039410, KIDNE20039940, KIDNE20040340, KIDNE20040540, KIDNE20040840, KIDNE20042620, KIDNE20042940, KIDNE20042950, KIDNE20043440, KIDNE20044110, KIDNE20045200, KIDNE20045340, KIDNE20045790, KIDNE20046810, KIDNE20048280, KIDNE20048640, KIDNE20048790, KIDNE20049810, KIDNE20050420, KIDNE20052960, KIDNE20053360, KIDNE20054000, KIDNE20054770, KIDNE20056290, KIDNE20056760, KIDNE20059800, KIDNE20059370, KIDNE20060140, KIDNE20060300, KIDNE20060530, KIDNE20060620, KIDNE20061490, KIDNE20062990, KIDNE20063530, KIDNE20063760, KIDNE20066520, KIDNE20067600, KIDNE20067750, KIDNE20068800, KIDNE20070050, KIDNE20070770, KIDNE20071860, KIDNE20073280, KIDNE20073520, KIDNE20073560, KIDNE20074220, KIDNE20075690, KIDNE20078110, LIVER10000790, MAMGL10000320, NB9N41000470, NT2NE200053710, NT2RI20006710, NT2RI20013420, NT2RI20016570, NT2RI20018460, NT2RI20025540, NT2RI20040590, NT2RI20085530, NT2RI20087490, NT2RI20087910, NT2RP60000350, NT2RP60001230, NT2RP70043730, NT2RP70069860, NT2RP70074220, OCBBF20014940, PLACE60020840, PLACE60043120, PROST10003430, SKNSH20001510, SMINT10000160, SPLEN20000470, SPLEN20001340, SPLEN20003570, STOMA10000470, TESTI10000700, TESTI20027070, TESTI20040310, TRACH10000300, TRACH20000790, TRACH20002500, TRACH20007800

[0255] The result of comparative analysis of cDNA libraries derived from liver tumor (TLIV) and normal liver (LIVER) showed that the genes whose expression levels were different between the two were the following clones (Table 10). FCBBF50002610, FEBRA20076220, KIDNE20033050, NT2NE20003840, KIDNE20062480, KIDNE20068800, LIVER10000580, LIVER10000670, LIVER10000790, LIVER10000990, LIVER10001040, LIVER10001110, LIVER10001750, LIVER10002300, LIVER10002780, LIVER10003030, LIVER10004330, LIVER10005420, LIVER20000330, FEBRA20004160, LIVER20004460, LIVER20005150, NT2NE20002140, NT2RI20030510, NT2RI20043040, NT2RI20090650, PROST10005640, PROST20032320, SALGL10001570, SMINT10000160, SPLEN20002420, TESTI20002530, TESTI20080200, THYMU10003590, TRACH20004720

[0256] The result of comparative analysis of cDNA libraries derived from lung tumor (TLUNG) and normal lung (HLUNG) showed that the genes whose expression levels were different between the two were the following clones (Table 11). NT2RI20030110, BNGH410001980, BRACE10000420, BRACE10001150, BRACE20014770, BRACE20018550, BRAWH20006970, BRAWH20014610, FEBRA20008810, FEBRA20015840, FEBRA20044120, HHDP20001490, HLUNG10000240, HLUNG10000300, HLUNG10000370, HLUNG10000640, HLUNG10000760, HLUNG10000990, HLUNG10001050, HLUNG10001100, HLUNG20000680, HLUNG20001160, HLUNG20001250, HLUNG20001420, HLUNG20001760, HLUNG20002550, HLUNG20003140, HLUNG20004120, HLUNG20004800, HLUNG20005010, HSYRA20014200, KIDNE20002660, KIDNE20033050, NT2NE20014350, NT2RI20016570, NT2RI20026540, NT2RI20051500, NT2RI20064120,

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NT2RI20083960, NT2RI20085260,
NT2RI20087490, NT2RP70009060, NT2RP70011660, NT2RP70029060, NT2RP70055020, NT2RP70074220,
NT2RP70076100, NTONG10002460, NTONG20008000, PLACE60043120, SKMUS20016340, SKNMC20005930,
SMINT20000180, SMINT20002390, SMINT20002770, SMINT20003960, STOMA10000470, STOMA200001880,
SYNOV20013740, TESTI20036250, TESTI20080200, TRACH20004610

[0267] The result of comparative analysis of cDNA libraries derived from ovary tumor (TOVER) and normal ovary (NOVER) showed the genes whose expression levels were different between the two were the following clones (Table 12).

BRACE20011880, TESTI20030710, BRACE20076210, NT2RI20053680, SKMUS20008630, TESTI20005910, TESTI20040310

[0268] The result of comparative analysis of cDNA libraries derived from stomach tumor (TSTOM) and normal stomach (STOMA) showed that the genes whose expression levels were different between the two were the following clones (Table 13).

HSYRA20011030, NT2RI20013420, NT2RP70079750, BRACE20003320, HEART20005060, HHDP20000950,
HLUNG20004120, HLUNG20005010, HSYRA20006400, KIDNE10000500, KIDNE20062480, NT2NE20053710,
NT2NE20054410, NT2RI20015400, NT2RI20016570, NT2RI20064120, NT2RI20070840, NT2RI20071330,
NT2RI20074980, NT2RI20077230, NT2RI20089420, NT2RP70000760, NT2RP70028750, PLACE60014430,
PLACE60024190, SKNMC20000970, STOMA10000470, STOMA10000520, STOMA10001170, STOMA10001330,
STOMA10001860, STOMA20000320, STOMA20000880, STOMA20001210, STOMA20001880, STOMA20002570,
STOMA20002890, STOMA20003960, STOMA20004780, STOMA20004820,
THYMU10003590

[0269] The result of comparative analysis of cDNA libraries derived from uterine tumor (TUTER) and normal uterus (UTERU) showed that the genes whose expression levels were different between the two were the following clones (Table 14).

NT2RI20085260, 3NB6920002810, BRACE10000420, BRACE20089990, BRACE20092120, BRAWH10001680,
BRAWH20011410, BRAWH20011660, FCBBF20005910, FCBBF50002610, FEBRA20005360, FEBRA20006800,
FEBRA20008800, FEBRA20044120, FEBRA20057520, HEART20005060, HHDP20000950, HLUNG10000760,
HLUNG20003140, HSYRA20014200,
HSYRA20014760, HSYRA20015800, IMR3210002420, IMR3220002230, IMR3220009350, IMR3220014350,
IMR3220016000, KIDNE20000850, KIDNE20060140, KIDNE20060300, MAMGL10000350, NT2NE20035690,
NT2NE20053710, NT2RI10000270, NT2RI20000640, NT2RI20002940, NT2RI20010910, NT2RI20013420,
NT2RI20016570, NT2RI20033380,
NT2RI20036950, NT2RI20037510, NT2RI20053350, NT2RI20057230, NT2RI20058110, NT2RI20071480,
NT2RI20074980, NT2RI20084810, NT2RI20087490, NT2RI20087910, NT2RP60000350, NT2RP70032030,
NT2RP70043730, NTONG10000980, NTONG10002460, PLACE60014430, PLACE60026880, PLACE60043960,
PLACE60044910, PLACE60047380,
PROST10002200, PROST10005280, PROST20025910, PROST20033380, PUAEN10000570, SALGL10001570,
SKMUS10000140, SKMUS20003430, SKMUS20009540, SKNMC10002510, SKNMC20000970, SKNSH10000860,
SMINT20002770, STOMA20003840, SYNOV20011440, TESTI10000230, TESTI20001820, TESTI20021490,
TESTI20080200, TESTI20082400,
TRACH10000300, TRACH200002370, TRACH20007800, TRACH20012890, UTERU10000770, UTERU10000960,
UTERU10001600, UTERU10001920, UTERU200004 UTERU20003380, UTERU20003930, UTERU20004850,
UTERU20005410, UTERU20005690

[0270] The result of comparative analysis of cDNA libraries derived from tongue cancer (CTONG) and normal tongue (NTONG) showed that the genes whose expression levels were different between the two were the following clones (Table 15).

3NB6910001160, 3NB6910001290, 3NB6910001730, BNGH42000470, BRACE20008850, BRACE20020910,
BRACE20074010, BRAWH20014840, BRAWH20089560, CTONG20003030, CTONG20005890, CTONG20007710,
CTONG20008270, CTONG20011390, CTONG20013200, CTONG20013660, CTONG20015330, CTONG20018200,
CTONG20019110, CTONG20019550, CTONG20020730, CTONG20021430, CTONG20024180, CTONG20024530,
CTONG20025580, CTONG20027210, CTONG20028030, CTONG20028160, CTONG20028200, CTONG20029650,
CTONG20037820, CTONG20047160, CTONG20055530, CTONG20064490, FEBRA20003770, FEBRA20004520,
FEBRA20007400, FEBRA20007570, FEBRA20012940, FEBRA20021940, FEBRA20044120, HCASM10001150,
HHDP20004560, HLUNG200003140, HSYRA20002480, IMR3220009350, IMR3220012180, KIDNE20000850,
KIDNE20002680, KIDNE20004220, KIDNE20005740, KIDNE20056760, KIDNE20060140, KIDNE20062480,
MESAN20000920, MESAN200003370, NHNPC20002060, NT2NE10001850, NT2NE20000560, NT2NE20002140,
NT2NE20003270, NT2NE20003840, NT2NE20014350, NT2NE20053710, NT2RI20000690, NT2RI20006710,
NT2RI20016570, NT2RI20018660, NT2RI20025300, NT2RI20025410, NT2RI20030190, NT2RI20030510,

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NT2RI20036950, NT2RI20046060, NT2RI20053350, NT2RI20067350, NT2RI20075720, NT2RI20078790, NT2RI20083960, NT2RI20087140, NT2RI20094060, NT2RP60000350, NT2RP60001230, NT2RP70000760, NT2RP70004770, NT2RP70009060, NT2RP70011660, NT2RP70023760, NT2RP70023790, NT2RP70024500, NT2RP70026190, NT2RP70029820, NT2RP70036470, NT2RP70043730, NT2RP70061880, NT2RP70071770, NT2RP70076100, NT2RP70079750, NT2RP70084870, NT2RP70093730, OCBBF20013070, PEBLM20003950, PLACE60037450, PLACE60043120, PROST10003430, PROST10005260, PROST20033230, PROST20033020, PROST20056040, SKNMC10002510, SKNMC20000650, SKNMC20010570, SKNSH20003470, SMINT20000180, SYN0V20013740, TESTI10000230, TESTI10001680, TESTI20007840, TESTI20021490, TESTI20022230, TESTI20023690, TESTI20030050, TESTI20042950, TESTI20068720, TESTI20080200, TRACH200012890, NT2RI20006980, NT2RI200092740, BRAWH20006970, FCBBF10007600, FEBRA20062700, IMR3220016000, KIDNE20073280, MAMGL10000350, NT2NE20035690, NT2RI20056470, NT2RI20058110, NT2RI20084810, NT2RI20085260, NT2RP70015910, NT2RP70036290, NT2RP70036320, NT2RP70074220, NT2RP70075370, NTONG10000330, NTONG10000520, NTONG10001230, NTONG10001300, NTONG10001820, NTONG10002140, NTONG10002460, NTONG10002570, NTONG10002640, NTONG20002650, NTONG20003340, NTONG20003630, NTONG20004920, NTONG20005830, NTONG20008000, NTONG20008780, NTONG20009660, NTONG20009850, NTONG20011370, NTONG20012220, NTONG20014280, NTONG20015500, NTONG20016120, OCBBF20011240, OCBBF20015860, PROST10002200, SKMUS200016340, SKNMC20000970, STOMA20004820, SYN0V10001280, SYN0V20011440, THYMU10000830, TRACH20000790, TRACH20009260

[0271] These genes are involved in cancers.

[0272] Further, there is a method to search for genes involved in development and differentiation: the expression frequency analysis in which the expression levels of genes are compared between developing or differentiating tissues and/or cells and adult tissues and/or cells. The genes involved in tissue development and/or differentiation are genes participating in tissue construction and expression of function, and thus are useful genes, which are available for regenerative medicine aiming at convenient regeneration of injured tissues.

[0273] Search was carried out for the genes whose expression frequencies were different between developing and/or differentiating tissues and/or cells, and adult tissues and/or cells, by using the information of gene expression frequency based on the database of the nucleotide sequences of 770,546 clones shown above.

[0274] The result of comparative analysis of cDNA libraries derived from fetal brain (FCBBF, FEBRA or OCBBF) and adult brain (BRAE, BRALZ, BRAMY, BRAWH, BRCAN, BRIOC, BRHIP, BRSSN, BRSTN or BRTHA) showed that the genes whose expression levels were different between the two were the following clones (Tables 16 to 36).

BRAE20002960, BRAE20074010, BRAE20077080, BRAE20077980, BRAE20083800, BRAE20088570, BRAWH10000010, BRAWH10000020, BRAWH10000070, BRAWH10000370, BRAWH10000940, BRAWH10001300, BRAWH10001640, BRAWH10001680, BRAWH10001740, BRAWH10001800, BRAWH20000340, BRAWH20000340, BRAWH20000480, BRAWH20000930, BRAWH20001770, BRAWH20002480, BRAWH20003230, BRAWH20004430, BRAWH20004760, BRAWH20005030, BRAWH20005540, BRAWH20006330, BRAWH20006510, BRAWH20006970, BRAWH20008660, BRAWH20008920, BRAWH20009010, BRAWH20009440, BRAWH20009840, BRAWH20011030, BRAWH20011290, BRAWH20011660, BRAWH20012030, BRAWH20014180, BRAWH20014380, BRAWH20014610, BRAWH20015030, BRAWH20036890, BRAWH20038320, BRAWH20047310, BRAWH20059980, BRAWH20060440, BRAWH20064930, BRAWH20066220, BRAWH20069600, BRAWH20069890, BRAWH20074060, BRAWH20076050, BRAWH20089560, BRAWH20092270, BRAWH20092610, BRAWH20093600, BRAWH20094850, IMR3220013170, KIDNE20000850, KIDNE20004220, KIDNE20031850, KIDNE20050420, MAMGL10000350, NT2NE20001740, NT2RI20042840, NT2RI20086560, NT2RP70002590, NT2RP70065270, NT2RP70074220, NTONG10001820, PEBLM20001470, PLACE60032040, SKMUS10000140, SMINT20005450, TESTI20004350, TESTI20008830, TRACH20007800, TRACH20016070, UMVEN20001330, 3NB6910001730, 3NB6920002810, ADRGL20000470, BNGH410001370, BNGH410001980, BRACE10000200, BRACE10000730, BRACE20000770, BRACE20001000, BRACE20001410, BRACE20002800, BRACE20003320, BRACE20005050, BRACE20005250, BRACE20005450, BRACE20005650, BRACE20005650, BRACE20005770, BRACE20006980, BRACE20007180, BRACE20008850, BRACE20009880, BRACE20010650, BRACE20010700, BRACE20011170, BRACE20011430, BRACE20011430, BRACE20011880, BRACE20013400, BRACE20013520, BRACE20013740, BRACE20013750, BRACE20014230, BRACE20014530, BRACE20014550, BRACE20014770, BRACE20014920, BRACE20015080, BRACE20015430, BRACE20016730, BRACE20016920, BRACE20017370, BRACE20018550, BRACE20018590, BRACE20018650, BRACE20018980, BRACE20021510, BRACE20021760, BRACE20022020, BRACE20022270, BRACE20024090, BRACE20024090, BRACE20024310, BRACE20024680, BRACE20024950, BRACE20025900, BRACE20026350, BRACE20026850,

	BRACE20027360,	BRACE20027250,	BRACE20027550,	BRACE20027270,	BRACE20027920,	BRACE20027990,
	BRACE20028120,	BRACE20028600,	BRACE20030780,	BRACE20032850,	BRACE20033190,	BRACE20033980,
	BRACE20034310,	BRACE20035160,	BRACE20035940,	BRACE20071380,	BRACE20071530,	BRACE20071970,
	BRACE20072010,	BRACE20072320,				
5	BRACE20072810,	BRACE20074470,	BRACE20075020,	BRACE20075270,	BRACE20075380,	BRACE20075630,
	BRACE20076210,	BRACE20076460,	BRACE20076630,	BRACE20076850,	BRACE20077610,	BRACE20077640,
	BRACE20077670,	BRACE20077840,	BRACE20078680,	BRACE20079020,	BRACE20079530,	BRACE20080970,
	BRACE20081140,	BRACE20083850,				
	BRACE20084430,	BRACE20084880,	BRACE20086530,	BRACE20086550,	BRACE20087080,	BRACE20087540,
10	BRACE20089600,	BRACE20089990,	BRACE20090140,	BRACE20091880,	BRACE20092120,	BRACE20092750,
	BRACE20093070,	BRACE20093110,	BRACE20094370,	CTONG20008270,	CTONG20013200,	CTONG20020730,
	CTONG20064490,	HDHPC20000950,				
	HDHPC20001150,	HDHPC200004560,	HSYRA200101780,	HSYRA200008280,	HSYRA200011530,	IMR320002660,
	IMR3220003020,	IMR3220009350,	KIDNE20003300,	KIDNE20004970,	KIDNE20005170,	KIDNE20009370,
15	KIDNE20068800,	KIDNE20073280,	LIVER20000370,	MESAN20002670,	NT2NE20005170,	NT2NE20011560,
	NT2NE20013640,	NT2NE20016970,				
	NT2RI20006710,	NT2RI20009740,	NT2RI20022430,	NT2RI20025300,	NT2RI20028020,	NT2RI20029260,
	NT2RI20030310,	NT2RI20030510,	NT2RI20040590,	NT2RI20044060,	NT2RI20049840,	NT2RI20049850,
	NT2RI20056470,	NT2RI20060720,	NT2RI20062100,	NT2RI20067350,	NT2RI20068250,	NT2RI20070840,
20	NT2RI20070960,	NT2RI20071480,				
	NT2RI20072540,	NT2RI20074980,	NT2RI20085260,	NT2RI20088120,	NT2RI20090660,	NT2RI20090830,
	NT2RP70013060,	NT2RP70013350,	NT2RP70023760,	NT2RP70024500,	NT2RP70030910,	NT2RP70036320,
	NT2RP70036470,	NT2RP70042350,	NT2RP70054930,	NT2RP70064900,	NT2RP70071140,	NT2RP70075370,
	NT2RP70076100,	NT2RP70079750,				
25	NT2RP70081370,	NT2RP70090120,	NT2RP70091490,	NT2RP70093730,	NTONG20014280,	NTONG20015500,
	PBLM10000340,	PLAC60014430,	PLAC60020840,	PLAC60024190,	PLAC60026920,	PLAC60030380,
	PLAC60038500,	PLAC60043970,	PROST10002720,	PROST20000530,	PROST20021620,	PROST20032320,
	PROST20033380,	PROST20062600,				
	SALGL10000050,	SALGL10001570,	SKMUS20000220,	SKMUS20001170,	SKMUS20002710,	SKMUS20009540,
30	SKMUS20011290,	SKMUS20015010,	SKMUS20015430,	SKMUS20016340,	SKNM20002240,	SKNM20015030,
	SKNSH20001510,	SMINT10001000,	SMINT20002390,	SPLN20001970,	STOMA20001210,	STOMA20002570,
	SYNOV20002910,	SYNOV20011440,				
	TEST110000510,	TEST110000700,	TESTH10001680,	TESTI20005200,	TESTI20015110,	TESTI20018290,
	TESTI20018690,	TESTI20018980,	TESTI20024670,	TESTI20032880,	TESTI20033250,	TESTI20036250,
35	TESTI20136910,	THYMU10000830,	THYMU10003020,	THYMU10003590,	UTERU10000960,	UTERU20005660,
	ADRLG10000650,	BGG120010970,				
	BRACE20004210,	BRACE20020500,	BRACE20020910,	BRACE20024780,	BRACE20028610,	BRACE20031010,
	BRACE20035270,	BRACE20035390,	BRACE20071740,	BRACE20077270,	BRAWH20001090,	CTONG20024530,
	CTONG20028200,	CTONG20055530,	FCBBF10005980,	FCBBF10006180,	FCBBF10006870,	FCBBF10006910,
40	FCBBF10007320,	FCBBF10007600,				
	FCBBF20000940,	FCBBF20001050,	FCBBF200001950,	FCBBF20002320,	FCBBF20002760,	FCBBF20005760,
	FCBBF20005910,	FCBBF20006770,	FCBBF20007330,	FCBBF20008080,	FCBBF20008150,	FCBBF20009400,
	FCBBF20009510,	FCBBF20012110,	FCBBF20012990,	FCBBF20014800,	FCBBF20017620,	FCBBF20017180,
	FCBBF20017200,	FCBBF40002820,				
45	HCASM10001150,	HDHPC20001490,	HLUNG10000640,	HLUNG20003140,	HLUNG20005010,	HSYRA20001350,
	HSYRA200014760,	HSYRA200163				

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	FEBRA20003110, FEBRA20003300, FEBRA20003780, FEBRA20003910, FEBRA20003970, FEBRA20003990, FEBRA20004040, FEBRA20004150, FEBRA20004540, FEBRA20004910, FEBRA20006560, FEBRA20006800, FEBRA20006900, FEBRA20007330, FEBRA20007400, FEBRA20007710, FEBRA20007720, FEBRA20007870, FEBRA20008090, FEBRA20008560, FEBRA20008800, FEBRA20008810, FEBRA20009590, FEBRA20009720, FEBRA20010930, FEBRA20011330, FEBRA20011460, FEBRA20012270, FEBRA20012940, FEBRA20013510, FEBRA20014870, FEBRA20015900, FEBRA20015910, FEBRA20017060, FEBRA20017900, FEBRA20019890, FEBRA20020860, FEBRA20024290, FEBRA20024420, FEBRA20027270, FEBRA20027830, FEBRA20028820, FEBRA20028970, FEBRA20029080, FEBRA20030540, FEBRA20031550, FEBRA20033080, FEBRA20034290, FEBRA20037070, FEBRA20041100, FEBRA20041910, FEBRA20042240, FEBRA20042370, FEBRA20042930, FEBRA20043290, FEBRA20044430, FEBRA20044900, FEBRA20045920, FEBRA20048180, FEBRA20050140, FEBRA20050790, FEBRA20052160, FEBRA20053770, FEBRA20053800, FEBRA20054270, FEBRA20057260, FEBRA20057520, FEBRA20059980, FEBRA20060920, FEBRA20061500, FEBRA20062700, FEBRA20063150, FEBRA20063540, FEBRA20064760, FEBRA20066670, FEBRA20067360, FEBRA20067930, FEBRA20068730, FEBRA20069420, FEBRA20070170, FEBRA20072000, FEBRA20072800, FEBRA20074140, FEBRA20075510, FEBRA20075680, HSYRA20006400, HSYRA20015800, IMR322002230, KIDNE20005740, KIDNE20053360, NT2NE20002140, NT2NE20003270, NT2NE20003840, NT2NE20007870, NT2NE200047160, NT2NE20053710, NT2RI20025410, NT2RI20051500, NT2RI20055640, NT2RI20058510, NT2RI20061830, NT2RI20064120, NT2RI20071330, NT2RI20075890, NT2RI20077230, NT2RI20094060, NT2RP70002380, NT2RP70009060, NT2RP70015910, NT2RP70094810, NT2RP70094980, PLACE60012810, PLACE60040050, SKMUS20008630, SKNMC20003050, SKNSH20003470, TESTI20003560, TESTI20012690, TESTI20030710, TESTI20082400, TRACH20009260, 3NB6910001160, 3NB6920015280, BRACE10000700, BRACE20019440, BRAWH20052250, KIDNE20045340, NT2NE20002590, NT2NE20014030, NT2RI20020220, NT2RI20026540, NT2RI20060710, NT2RI20083960, NT2RI20084810, NT2RP70011660, NT2RP70021510, NT2RP70024490, NT2RP70026190, NT2RP70039600, NT2RP70049250, NT2RP70071770, NT2RP70093940, NTONG10002640, NTONG20002650, OCBBF10000420, OCBBF10000670, OCBBF10000860, OCBBF10000910, OCBBF10001040, OCBBF10001180, OCBBF10001190, OCBBF10001220, OCBBF20002770, OCBBF20002870, OCBBF20007190, OCBBF20008240, OCBBF20009980, OCBBF20010750, OCBBF20011010, OCBBF20011400, OCBBF20011760, OCBBF20014080, OCBBF20014940, OCBBF20015270, OCBBF20015280, OCBBF20015860, OCBBF20017080, PLACE60043960, SMINT20002770, TESTI20001790, TESTI20007840, TESTI20009700, TESTI20027070, TESTI20053960, TRACH20000790, 3NB6920010220, BRACE10001870, BRAWH20004480, BRAWH200040950, FEBRA20011970, KIDNE20062480, NT2RI20029580, NT2RI20035560, NT2RI20043980, NT2RP70000760, NT2RP70042040, NT2RP70069860, NT2RP70088550, OCBBF20001260, TESTI10000230, 3NB6920017190, ADRGL10000020, BRACE10001660, BRAWH10001620, CTONG20028030, KIDNE20004030, KIDNE20060300, NB9N420000420, NT2NE20000560, NT2NE20004070, NT2NE20007630, NT2RI20004120, NT2RI20013420, NT2RI20033380, NT2RI20036950, NT2RI20053350, NT2RI20053680, NT2RI20078840, NT2RI20083360, NT2RI20090650, NT2RP60001090, NT2RP70004770, NT2RP70023790, NT2RP70055200, NT2RP70085570, NTONG10000980, NTONG20016120, OCBBF20011240, OCBBF20012100, OCBBF20013070, OCBBF20014020, PEBLM20003950, PLACE50001130, PLACE60021510, PUAEN10000570, SKNMC20000970, TESTI20040310, TRACH20004610, 3NB6920005450, BRACE10000420, BRACE20076410, BRACE20078820, BRAWH20006860, BRAWH20089030, FCBBF1000067 FCBBF10006860, FCBBF20015380, FCBBF50002610, FEBRA20004520, FEBRA20005360, FEBRA20009010, FEBRA20014920, FEBRA20015840, FEBRA20021910, FEBRA20021940, FEBRA20043250, FEBRA20057780, FEBRA20057880, FEBRA20066270, FEBRA20074580, HHDP200000550, HSYRA20015740, HSYRA20016210, IMR3210002420, IMR3220018000, KIDNE20060140, MAMGL10000320, NT2NE20008090, NT2NE20014350, NT2RI20000640, NT2RI20002940, NT2RI20015400, NT2RI20033830, NT2RI20037510, NT2RI20057230, NT2RI20087910, NT2RI20089420, NT2RP70043730, NT2RP70047900, PLACE60043120, PROST20033020, SYNOV10001280, TESTI20021490, THYMU20002360, TRACH20012890, 3NB6910001290, BNGH420004740, BRACE20034490, BRAWH20005220, FEBRA20003770, FEBRA20007570, FEBRA200008740, FEBRA20012450, FEBRA20012450, FEBRA20017150, FEBRA20025250, FEBRA20044120, FEBRA20076220,	
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HSYRA20002480, IMR3220014350, MESAN20001490, NHNPC20002060, NT2NE10000180, NT2NE20003920, NT2RI200006690, NT2RI20013850, NT2RI20014500, NT2RI20025540, NT2RI20030310, NT2RI20075720, NT2RP60000350, NT2RP60001230, NT2RP70028750, NT2RP70029060, NT2RP70032030, NTONG20003340, OCBBF20000130, OCBBF20002310,

5 OCBBF20009040, SKNMC20000650, SMINT20003960, TESTI20026320, TESTI20080200

[0275] The result of comparative analysis of cDNA libraries derived from fetal heart (FEHRT) and adult heart (HEART) showed that the genes whose expression levels were different between the two were the following clones (Table 37): KIDNE20062480, NT2RI20033040, NT2RP60000350, BGGH120010970, BRACE10000420, BRACE10001150, BRACE20003320, BRACE20077980, BRAWH10000370, BRAWH20000340, BRAWH20011660, BRAWH20014840, 10 FEBRA20008740, FEBRA20072800, HEART20000350, HEART20000990, HEART20003090, HEART20004110, HEART20004480, HEART20004920, HEART20005060, HEART20005200, HEART20005680, HHDP20001150, HLUNG20005010, HSYRA20014200, IMR3220013170, KIDNE20004970, NT2RI20000640, NT2RI20006710, NT2RI20015400, NT2RI20026540, NT2RI20037510, NT2RI20057230, NT2RI20064120, NT2RI20071330, NT2RI20071480, NT2RI20077540,

15 NT2RI20084810, NT2RI20087910, NT2RP70000760, NT2RP70024500, NT2RP70029080, NTONG10001820, PLACE60012810, PLACE60043120, PROST20000530, SKMUS10000640, SKMUS20004580, SKMUS20015010, SMINT20002770, TESTI20033250, TESTI20074640, UMYEN20001330

[0276] The result of comparative analysis of cDNA libraries derived from fetal kidney (FEKID) and adult kidney (KIDNE) showed that the genes whose expression levels were different between the two were the following clones (Table 38).

20 3NB692003300, 3NB6920009120, BGGH120010970, BRACE20004210, BRACE20005250, BRACE20011170, BRACE20020910, BRACE20026850, BRACE20080970, BRAWH20000340, BRAWH20006970, BRAWH20011660, FCBF20001950, FEBRA20021940, FEBRA20043250, HLUNG10000540, IMR3220007420, IMR3220014350,

25 KIDNE10000280, KIDNE10000500, KIDNE10001040, KIDNE10001430, KIDNE10001450, KIDNE10001520, KIDNE20000410, KIDNE20000510, KIDNE20000700, KIDNE20000850, KIDNE20001670, KIDNE20001920, KIDNE20002440, KIDNE20002450, KIDNE20002680, KIDNE20003150, KIDNE20003300, KIDNE20003490, KIDNE20003750, KIDNE20004030, KIDNE20004220, KIDNE20004970,

30 KIDNE20005130, KIDNE20005170, KIDNE20005190, KIDNE20005740, KIDNE20031850, KIDNE20033050, KIDNE20033350, KIDNE20033570, KIDNE20033730, KIDNE20033770, KIDNE20037520, KIDNE20039410, KIDNE20039940, KIDNE20040340, KIDNE20040540, KIDNE20040840, KIDNE20044260, KIDNE20042940, KIDNE20042950, KIDNE20043440,

35 KIDNE20045200, KIDNE20045340, KIDNE20045790, KIDNE20046810, KIDNE20048280, KIDNE20048640, KIDNE20048790, KIDNE20049810, KIDNE20050420, KIDNE20052960, KIDNE20053360, KIDNE20054000, KIDNE20054770, KIDNE20056290, KIDNE20056760, KIDNE20059080, KIDNE20059370, KIDNE20060140, KIDNE20060300, KIDNE20060530,

40 KIDNE20060820, KIDNE20061490, KIDNE20062480, KIDNE20062990, KIDNE20063530, KIDNE20063760, KIDNE20066520, KIDNE20067600, KIDNE20067750, KIDNE20068800, KIDNE20070050, KIDNE20070770, KIDNE20071860, KIDNE20073280, KIDNE20073520, KIDNE20073560, KIDNE20074220, KIDNE20075590, KIDNE20078100, KIDNE20078110,

45 LIVER10000790, MAMGL10000320, NB9N410000470, NT2NE20053710, NT2RI20006710, NT2RI20013420, NT2RI20016570, NT2RI20018460, NT2RI20025540, NT2RI20040590, NT2RI20085530, NT2RI20087490, NT2RI20087910, NT2RP60000350, NT2RP60001230, NT2RP70043730, NT2RP70069850, NT2RP70074220, OCBBF20014940, PLACE60014430,

50 PLACE60020840, PLACE60043120, PROST10003430, SKNMC20000970, SKNSH20001510, SMINT10000160, SMINT20003960, SPLEN20000470, SPLEN20001340, SPLEN20003570, STOMA10000470, SYNOV10001280, TESTI20007000, TESTI20027070, TESTI20040310, TRACH10000300, TRACH20000790, TRACH20002500, TRACH20007800, KIDNE10000080, KIDNE20044110, NT2RI20033040, NT2RI20037510, NT2RP70065270, TRACH20012890

[0277] The result of comparative analysis of cDNA libraries derived from fetal lung (FELNG) and adult lung (HLUNG) showed that the genes whose expression levels were different between the two were the following clones (Table 39): BNGH410001980, BRACE10000420, BRACE10001150, BRACE20014770, BRACE20018550, BRAWH20006970, BRAWH20014610, FEBRA200008810, FEBRA20015840, FEBRA20044120, HHDP200001490, HLUNG10000240, 55 HLUNG10000300, HLUNG10000370, HLUNG10000640, HLUNG10000750, HLUNG10000990, HLUNG10001050, HLUNG10001100, HLUNG20000680, HLUNG20001160, HLUNG20001250, HLUNG20001420, HLUNG20001760, HLUNG20002550, HLUNG20003140, HLUNG20004120, HLUNG20004800, HLUNG20005010, HSYRA20014200, KIDNE20002660, KIDNE20033050,

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NT2NE20014350, NT2RI20016570, NT2RI20026540, NT2RI20051500, NT2RI20084120, NT2RI20083960, NT2RI20085260, NT2RI20087490, NT2RP70009060, NT2RP70011660, NT2RP70029060, NT2RP70055020, NT2RP70074220, NT2RP70076100, NTONG10002460, NTONG20008000, PLACE60043120, SKMUS20016340, SKNMC20005930, SMINT20000180, SMINT20002390, SMINT20002770, SMINT20003960, STOMA10000470, STOMA20001880, SYNOV20013740, TESTI20036250, TESTI20080200,

TRACH20004610, BRACE20004210, IMR3220007420

[0278] These genes are involved in regeneration of tissues and/or cells.

EXAMPLE 8

Expression frequency analysis by PCR

[0279] Specific PCR primers were prepared based on the full-length nucleotide sequences, and the expression frequency was analyzed by the ATAC-PCR method (Adaptor-tagged competitive PCR method: Nucleic Acids Research 1997, 25(22): 4694-4696; "DNA Micro-array and Advanced PCR Techniques", Cell Technology, supplement, Eds., Muramatsu and Nawa (Shujunsha, 2000): 104-112). Inflammation-related genes can be identified by revealing the genes whose expression levels are altered depending on the presence of an inflammation-inducing factor. Then, by using THP-1 cell line, which is a cell line of monocyte line, and TNF- α and LPS, both of which are inflammation-inducing factors, suitable for this system, the genes whose expression levels are altered depending on the presence of the factors were searched for by the system.

[0280] THP-1 cell line (purchased from DAINIPPON PHARMACEUTICAL) was cultured to be confluent in RPMI1640 medium (sigma) containing 5% fetal calf serum (GIBCO BRL). Then, the medium was changed with the medium containing 10 ng/ml TNF- α (human recombinant TNF- α ; Pharmacia Biotech) or 1 μ g/mL LPS (Lipopolysaccharides; sigma), and the culture was continued at 37°C under 5% CO₂. After three hours, the cells were harvested, and total RNA was extracted from them by using ISOGEN reagent (Nippon Gene). The extraction was carried out according to the method in the document attached to ISOGEN reagent. In addition, total RNA was also extracted from the cells cultured without stimulation of TNF- α or LPS.

[0281] The genes involved in the onset of gastritis and gastroduodenal ulcer induced by the infection of *Helicobacter pylori* to the epithelia of stomach can be identified by revealing the genes whose expression levels are altered depending on co-culturing the cells with *Helicobacter pylori*. Then, by using co-culture of a gastric cancer cell line with *Helicobacter pylori*, suitable for this system, the genes whose expression levels are altered depending on the presence of *Helicobacter pylori*, were searched for by the system.

[0282] A gastric cancer cell line MKN45 (provided by the Cell Bank, RIKEN GENE BANK, The Institute of Physical and Chemical Research) was cultured to be confluent in RPMI1640 medium (sigma) containing 10% fetal calf serum (GIBCO BRL). Then, the medium was changed with the medium containing 100-fold excess (in terms of the number of cells or the number of colonies) of *Helicobacter pylori* (TN2 strain: provided by Prof. Omata, Faculty of Medicine, The University of Tokyo), as compared with the number of the cancer cells. The culture was continued at 37°C under 5% CO₂. After three hours, the cells were harvested, and total RNA was extracted from them by using ISOGEN reagent (Nippon Gene). The extraction was carried out according to the method in the document attached to ISOGEN reagent. In addition, total RNA was also extracted from the cells cultured without *Helicobacter pylori*.

[0283] The analysis by the ATAC-PCR method was carried out basically according to "DNA Micro-array and Advanced PCR Techniques", Cell Technology, supplement (Genome Science Series 1, Eds., Muramatsu and Nawa (Shujunsha, 2000): 104-112). Adapter ligation to the internal standard sample (sample to make the calibration curve for the clone of interest) and test sample was carried out in the two separate reaction systems indicated below. The combination of 6 types of adapters (AD-1, AD-2, AD-3, AD-4, AD-5 and AD-6: see the sequences indicated below) and the samples are as follows.

Reaction system A

AD1; internal standard, 10-fold
AD2; THP-1 cells, unstimulated
AD3; internal standard, 3-fold
AD4; THP-1 cells, TNF- α stimulation
AD5; THP-1 cells, LPS stimulation
AD6; internal standard, 1-fold

Reaction system B

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AD1; internal standard, 1-fold
 AD2; MKN45 cells, unstimulated
 AD3; internal standard, 3-fold
 AD4; MKN45 cells, co-cultured with *Helicobacter pylori*
 AD5; internal standard, 10-fold

Adaptor sequences:

AD1;
 SEQ ID NO: 3283//5'-GTACATATTGTCGTTAGAACGCG-3'
 SEQ ID NO: 3284//3'-CATGTATAACAGCAATCTTGC GCCTAG-5'
 AD2;
 SEQ ID NO: 3285//5'-GTACATATTGTCGTTAGAACGCGACT-3'
 SEQ ID NO: 3286//3'-CATGTATAACAGCAATCTTGC GCCTAG-5'
 AD3;
 SEQ ID NO: 3287//5'-GTACATATTGTCGTTAGAACGCGCATACT-3'
 SEQ ID NO: 3288//3'-CATGTATAACAGCAATCTTGC GCCTAG-5'
 AD4;
 SEQ ID NO: 3289//5'-GTACATATTGTCGTTAGAACGCGATCCATACT-3'
 SEQ ID NO: 3290//3'-CATGTATAACAGCAATCTTGC GCCTAG-5'
 AD5;
 SEQ ID NO: 3291//5'-GTACATATTGTCGTTAGAACGCGCTCAATCCATACT-3'
 SEQ ID NO: 3292//3'-CATGTATAACAGCAATCTTGC GCAGTTAGGTATGACTAG-5'
 AD6;
 SEQ ID NO: 3293//5'-GTACATATTGTCGTTAGAACGCGTACTCAATCCATACT-3'
 SEQ ID NO: 3294//3'-CATGTATAACAGCAATCTTGC GCATGAGTTAGGTATGACTAG-5'

[0284] The internal standard sample used for this assay was a mixture of total RNAs of THP-1 Control, MKN45 Control, NT2 (Stratagene; catalog No. 204101). RNA preparation from the culture cells was carried out according to the standard method.

[0285] The sequences of primers specific to the genes and the names of clones of interest in the analysis are as follows. The gene specific primers were designed to produce the PCR products of 70 to 200 bp, which are derived from the adaptor-containing cDNA. The sequence of adaptor-specific primer (labeled with fluorescence (FAM)) used in the competitive PCR was GTACATATTGTCGTTAGAACGCG (22 nucleotides; SEQ ID NO: 3295). PCR was basically carried out with a cycling profile of preheating at 94°C for 3 minutes, and 30 cycles of denaturation at 94°C for 30 seconds/annealing at 50°C for 60 seconds/extension at 72°C for 90 seconds; in some cases, merely the annealing temperature was changed.

The nucleotide sequences of clone specific primers used in the experiments

[0286] Clone name, primer sequence and SEQ ID NO are indicated below in this order. Each is demarcated by a double slash mark (/).

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3NB6920000290//CTCCTCCAGCAGAACTTG//SEQ ID NO: 3296
ADRL10000180//TTTAGAGCTGATCCCCATT//SEQ ID NO: 3297
5 BNGH410001370//TAAAGCAGGAAATTGTAAA//SEQ ID NO: 3298
BRACE10001590//ATATGGACAAAGGACCAATT//SEQ ID NO: 3299
BRACE10001690//AGGACTAGATTCACGTGCTTA//SEQ ID NO: 3300
10 BRACE20010650//CAACTCTCAACACCACAATC//SEQ ID NO: 3301
BRACE20013400//CTACTCAAGGACAGCCACAC//SEQ ID NO: 3302
BRACE20030780//AGATAGAGGCTTGCTGGTGT//SEQ ID NO: 3303
BRACE20034490//CCTTATGTCAAACATGCGATT//SEQ ID NO: 3304
15 BRACE20077640//TTTGCCATTATTCATTGGTTG//SEQ ID NO: 3305
BRACE20079530//GTAATATCACCCACAGAGG//SEQ ID NO: 3306
BRACE20083850//TATCATCTTTTGGGGCTTTG//SEQ ID NO: 3307
20 BRACE20091880//AATAAGCCAGTTGCATCCTC//SEQ ID NO: 3308
BRAWH10001620//TCTCTCATCTCCAACATGC//SEQ ID NO: 3309
BRAWH20004430//TGAATTGAAAGAGACACACT//SEQ ID NO: 3310
25 FCBBF10006180//CTTAATCCAGTTCATCAGCT//SEQ ID NO: 3311
FEBRA20003780//TTTTGAGACAGAGTTTCGCT//SEQ ID NO: 3312
FEBRA20006800//ATGTTTACGATTGCCTTTG//SEQ ID NO: 3313
30 FEBRA20008810//GAAGCATCTTTGGTGTACTA//SEQ ID NO: 3314
FEBRA20012940//TGTCCTGGAAAGTAATATA//SEQ ID NO: 3315
FEBRA20015840//AACACAGTAGCCAGAACAG//SEQ ID NO: 3316
HCASM10000610//AAGAGCCTACTACAGCCAG//SEQ ID NO: 3317
35 HEART20000350//TTTAAGAGCACACAGAAGTC//SEQ ID NO: 3318
HEART20004480//ATTACTGGTGTGGAGTGGGT//SEQ ID NO: 3319
HEART20005060//ACTCTGCCTTCACTTTCCTT//SEQ ID NO: 3320
40 HHDP20000950//GATAAAGGATACAGCCAAAA//SEQ ID NO: 3321
HLUNG10000370//ATCATGTGTCGTACAGAATT//SEQ ID NO: 3322
HLUNG20001160//ACTGCCTTCAATCTCAGGTT//SEQ ID NO: 3323
45 HLUNG20001760//ATCACTGCCAATTTACAAA//SEQ ID NO: 3324
HSYRA20003470//CCACCGAGTTCTGTG//SEQ ID NO: 3325
HSYRA20013320//GTCATGGCCACAGTTGTATC//SEQ ID NO: 3326

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IMR3210001580//GATAAAGGATACAGCCAAAA//SEQ ID NO: 3327
IMR3210002660//CCCAAAATGTGTATTATTCA//SEQ ID NO: 3328
5 IMR3220008380//TTCGGCAATAATCTTCTCTT//SEQ ID NO: 3329
IMR3220008590//CCACCAACACTTAGACATCA//SEQ ID NO: 3330
KIDNE10001520//GAATTATAGGTGCACAACAC//SEQ ID NO: 3331
10 KIDNE20000850//TCTTCTAGTGGAAGAGGTTTA//SEQ ID NO: 3332
KIDNE20003490//TATCTGAAATGTGTTTGGT//SEQ ID NO: 3333
KIDNE20005170//ACTCCTGGCTTCTATTTC//SEQ ID NO: 3334
15 KIDNE20033730//GACAGTCTCGCTGTATCTCC//SEQ ID NO: 3335
KIDNE20040540//ACATCCAGTACACCTTCTCC//SEQ ID NO: 3336
KIDNE20050420//GTCGAAAGTGTGCTCCTAG//SEQ ID NO: 3337
KIDNE20061490//TCATAGCTGAGGGGTTAAGT//SEQ ID NO: 3338
20 KIDNE20062990//ATAGCTCTTGTTCAGTGTG//SEQ ID NO: 3339
LIVER20000330//AAGCATGTGGGAGTTATTTA//SEQ ID NO: 3340
NT2NE10001630//CTTGAGAGTCCAGGTTTCCT//SEQ ID NO: 3341
25 NT2NE10001850//CCCATAAAGAATAGAAGCTC//SEQ ID NO: 3342
NT2NE20003920//CTCATGGGGCTAAGTCTATT//SEQ ID NO: 3343
NT2NE20005500//TCAAAGTCCAGGATAGCATT//SEQ ID NO: 3344
30 NT2RI20009740//ACTGATTGGTTCTGCGATT//SEQ ID NO: 3345
NT2RI20014500//CTTACTTCGAGTTCTAGCAC//SEQ ID NO: 3346
NT2RI20016570//TGCTGCTCATGTTAAACTTG//SEQ ID NO: 3347
NT2RI20018660//AAACATCATCTCTTCTCTGG//SEQ ID NO: 3348
35 NT2RI20021520//GCTGAAGAGACAATAAGTC//SEQ ID NO: 3349
NT2RI20050870//GACAGAGTAGTGGGGCATCT//SEQ ID NO: 3350
NT2RI20053350//TTCAGCAGGTAGACAACATC//SEQ ID NO: 3351
40 NT2RI20070480//CCTCTCTTCAGTTGAGCAT//SEQ ID NO: 3352
NT2RI20073030//GGGCTTGTTTTACGC//SEQ ID NO: 3353
NT2RI20078270//CCTAGGCAGTAACATGAAAA//SEQ ID NO: 3354
45 NT2RI20078790//GCAGACAGGTACAGCTGAGT//SEQ ID NO: 3355
NT2RI20083360//TTATTTTGTATTACCTTGGA//SEQ ID NO: 3356
NT2RP60000080//ACTGTAATCTCCTTGCCCT//SEQ ID NO: 3357
NT2RP60000390//GAGTTTGGGGACAGTCAAGT//SEQ ID NO: 3358
50 NT2RP60000590//AAATGCAAAATTGCTGAGAT//SEQ ID NO: 3359
NTONG10000980//TTCAGCAGGTAGACAACATC//SEQ ID NO: 3360
NTONG10002570//GTCGCTGAAATTGCTTCTT//SEQ ID NO: 3361
55 PLACE60020160//CCATATCCACTTTCATCATC//SEQ ID NO: 3362

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PLACE60026990//CAAGAACTGACAATCACGG//SEQ ID NO: 3363
 PLACE60047380//AAGGAGTTGACATTTTGTCTG//SEQ ID NO: 3364
 5 PUAEN10003220//TTTTTCAGAGGGCTTTGTGT//SEQ ID NO: 3365
 SKNMC10000290//ATAACTGAACCCATGGAAAG//SEQ ID NO: 3366
 SKNMC10001590//ACATCCAGTACACCTTCTCC//SEQ ID NO: 3367
 10 SKNMC20000650//GCATAGGAGACTGTCAAAA//SEQ ID NO: 3368
 STOMA20002570//GGTATCTTGGAGCTCCTCAG//SEQ ID NO: 3369
 STOMA20002890//GTCAGCATCTACTCTGGGTC//SEQ ID NO: 3370
 15 SYN0V20001770//AAGAAATAAACACACGAAAA//SEQ ID NO: 3371
 TESTI10000230//AAATGCAAAATTGCTGAGAT//SEQ ID NO: 3372
 TESTI10000550//CAGAACACTCCTCATACCTC//SEQ ID NO: 3373
 TESTI20011340//AAAGTACAGCAGAAGATGGG//SEQ ID NO: 3374
 20 THYMU10005580//AACAGCTTCTTCATCACAGT//SEQ ID NO: 3375
 TRACH10000630//ATAGAGGAAGGTGGCAACTG//SEQ ID NO: 3376
 TRACH20001960//CTCTTTTCCATCACATTTCCC//SEQ ID NO: 3377
 25 UMVEN10001220//CCAAGTTCTCATTTCCACAT//SEQ ID NO: 3378
 UMVEN20001330//AGCTAACAGGTTTTCACAC//SEQ ID NO: 3379
 UTERU20004850//AGACTGGGTCTTGCCATACT//SEQ ID NO: 3380

[0287] The result of expression frequency analysis is shown in Table 40. The clones not shown in the table contain clones whose expression levels could not be measured because the levels were too low or the sizes of the PCR products were different from the expected. It was confirmed that the expression levels of TNF- α , IL-1, and IL-8 genes used as positive control genes were elevated.

[0288] The result obtained by the search for the genes whose expression levels were altered depending on the presence of TNF- α or LPS in culturing THP-1 cell, which is a human monocyte cell line, showed that the clones whose expression levels were elevated by twofold or more depending on the TNF- α stimulation (the clones whose expression levels were 0.1 or lower both before and after the stimulation were excluded), were

ADRL1000180, BRACE20030780, BRACE20077640, BRACE20083850, BRAWB20004430, FCBBF10006180, FEBRA20003780, FEBRA20006800, FEBRA20012940, FEBRA20015840, HEART20004480, HLUNG10000370, HLUNG20001160, HSYRA20013320, IMR3220008380, KIDNE10001520, KIDNE20040540, KIDNE20061490, KIDNE20062990, NT2NE10001630, NT2NE20003920, NT2NE20005500, NT2RI20014500, NT2RI20016570, NT2RI20078270, NT2RI20083360, NTONG10002570, PUAEN10003220, SKNMC10000290, STOMA20002570, TESTI20011340, UTERU20004850.

[0289] Further, the clones whose expression levels were elevated by twofold or more depending on the LPS stimulation (the clones whose expression levels were 0.1 or lower both before and after the stimulation were excluded), were FCBBF10006180, FEBRA20015840, HLUNG10000370, HLUNG20001160, HSYRA20013320, KIDNE20040540, KIDNE20061490, NT2NE10001630, NT2NE20003920, NT2NE20005500, NT2RI20014500, NT2RI20016570, NT2RI20078270, NTONG10002570, PUAEN10003220, STOMA20002570, TESTI20011340. These genes whose expression levels were elevated by LPS stimulation, were all up-regulated by the TNF- α stimulation.

[0290] On the other hand, with respect to the genes whose expression is suppressed, in particular cases where the expression levels were relatively high in the unstimulated cells (the relative value were 1 or higher), the clones whose expression levels were decreased by twofold or more by the TNF- α stimulation, were BRACE20013400, BRACE20091880, HEART20005060, HLUNG20001760, IMR3220008590, NT2NE10001850, NT2RI20018660, NT2RI20053350, NT2RI20070480, PLACE60047380, STOMA20002890, SYN0V20001770, TRACH20001960. Further, when the levels were normalized by using the ratio of the expression level of β -actin widely used in data normalization for gene expression level, the clones whose expression levels were decreased by tenfold or more depending on the LPS stimulation, were BRACE20013400, BRACE20091880, HEART20005060, HLUNG20001760,

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NT2R120070480, UMVEN20001330. Among the genes whose expression levels were decreased by TNF- α stimulation, the genes whose expression levels were also decreased by the LPS stimulation were BRACE20013400, BRACE20091880, HEART20005060, HLUNG20001760, NT2R120070480.

[0291] These clones were thus revealed to be involved in the inflammation reaction induced by TNF- α or LPS.

[0292] The result obtained by the search for the genes whose expression levels were altered depending on co-culturing gastric cancer cell line MKN45 with *Helicobacter pylori*, showed that the clones whose expression levels were elevated by twofold or more depending on the presence of *Helicobacter pylori* (the clones whose expression levels were 0.1 or lower both before and after the stimulation were excluded), were BRACE10001590, BRACE20079530, BRAWH10001620, FEBRA20006800, KIDNE20003490, KIDNE20040540, KIDNE20050420, NT2NE10001850, STOMA20002890, SYNOV20001770. TEST110000550, UTERU20004850. Of the clones, FEBRA20006800, KIDNE20040540 and UTERU20004850 were also up-regulated by TNF- α stimulation in the human monocyte cell line THP-1.

[0293] On the other hand, with respect to the genes whose expression is suppressed, in particular cases where the expression levels were relatively high in the unstimulated cells in (the relative value were 1 or higher), when the levels were normalized by using the ratio of the expression level of β -actin widely used in data normalization for gene expression level, the clones whose expression levels were decreased by fivefold or more in the presence of *Helicobacter pylori*, were BRACE20034490, BRACE20077640, BRACE20083850, KIDNE20005170, LIVER20000330, NT2RP60000390, NTONG10000980, UMVEN20001330.

[0294] These clones are involved in gastritis or gastroduodenal ulcer.

Table 3

Clone ID	CD34C	D30ST	D60ST	D90ST
KIDNE20062480	0	4.908	0	5.748
NT2R120016570	0	7.035	0	8.24
PLACE60020840	0	8.776	0	20.558
3NB6920002810	0	0	0	4.74
BRAGE20035270	0	0	0	33.245
BRAWH20000340	0	0	0	40.521
FEBRA20062700	0	0	0	35.533
HSYRA20011030	0	0	0	9.617
NT2RP70030910	0	0	0	39.804
OCBBF20011240	0	0	0	44.145
PLACE60043120	0	0	0	15.442
SYNOV20011440	0	0	0	15.55
HCASM10001150	0	0	40.145	0
IMR3220016000	0	0	13.886	0
NT2R120082210	0	0	79.241	0
D30ST20001840	0	100	0	0
FEBRA20012940	0	37.059	0	0
FEBRA20021910	0	63.399	0	0
IMR3220002230	0	10.991	0	0
IMR3220012180	0	18.197	0	0
NT2R120000640	0	9.996	0	0
NT2R120010910	0	46.971	0	0
NT2R120058110	0	20.306	0	0
NT2RP60000350	0	4.385	0	0
NT2RP70011660	0	8.936	0	0
PEBLM20003950	0	14.226	0	0
PLACE60049310	0	68.294	0	0
PROST2006260	0	66.053	0	0
TEST120007840	0	7.864	0	0
TEST120040310	0	8.52	0	0
TEST120080200	0	4.493	0	0

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Table 3 (continued)

Clone ID	CD34C	D30ST	D60ST	D90ST
THYMU10003590	0	9.698	0	0
TRACH10000630	0	34.338	0	0
TRACH20007800	0	18.508	0	0
CD34C20000510	100	0	0	0
HSYRA20016210	5.607	0	0	3.6
KIDNE20004030	66.99	0	0	0
KIDNE20073280	54.663	0	0	0
NT2RP70055020	58.521	0	0	0
PLACE60043960	58.654	16.078	0	0
SKMUS10000220	57.743	0	0	0

Table 4

Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
SKNMC20000970	19	2.312	0.784	1.188
3NB6920009120	0	2.916	1.978	8.993
BRAWH20006970	0	4.004	2.717	4.117
KIDNE20062480	0	1.503	7.137	3.09
NHNPC20002060	0	1.674	1.136	5.165
NT2NE20053710	0	7.977	0.773	2.343
NT2R12000640	0	1.53	1.038	3.147
NT2R120004210	0	29.541	40.087	30.373
NT2R120006710	0	2.481	1.683	2.551
NT2R120009740	0	13.985	9.489	14.379
NT2R120013420	0	4.074	1.382	2.094
NT2R120013850	0	6.297	4.273	2.158
NT2R120014100	0	53.957	18.305	27.738
NT2R120025410	0	17.546	11.905	18.04
NT2R120033040	0	3.342	3.401	3.436
NT2R120035560	0	28.514	3.869	5.864
NT2R120036950	0	4.691	9.549	4.823
NT2R120051500	0	3.392	9.205	10.462
NT2R120053350	0	2.329	1.581	2.395
NT2R120057230	0	2.418	1.641	7.458
NT2R120071330	0	13.599	9.227	6.991
NT2R120075720	0	4.321	2.932	4.443
NT2R120083960	0	8.389	5.692	8.625
NT2R120087910	0	5.711	1.938	2.936
NT2R120090650	0	2.967	6.039	3.051
NT2R120094060	0	26.699	18.115	13.726
NT2RP60000350	0	5.37	4.554	4.141
NT2RP70000760	0	4.602	3.122	4.732
NT2RP70036800	0	6.556	8.897	6.741
NT2RP70071770	0	18.93	6.422	9.732
NT2RP70074220	0	4.004	2.717	4.117
TESTI20007840	0	19.261	3.267	4.951
TESTI20080200	0	1.375	1.867	1.414
3NB6920002810	0	1.239	0.841	0
3NB6920005450	0	7.198	4.884	0

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Table 4 (continued)

Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
5	HSYRA20015740	0	8.09	5.489
	HSYRA20016210	0	2.353	1.277
	IMR3220016000	0	1.458	0.989
	KIDNE20060140	0	14.005	9.502
	NT2RI20014490	0	29.632	70.368
10	NT2RI20015950	0	59.577	40.423
	NT2RI20022520	0	59.577	40.423
	NT2RI20025170	0	59.577	40.423
	NT2RI20025540	0	5.634	3.823
	NT2RI20030510	0	15.012	10.186
15	NT2RI20040590	0	13.827	9.381
	NT2RI20046060	0	9.661	13.11
	NT2RI20053680	0	3.443	4.672
	NT2RI20058510	0	12.325	16.726
20	NT2RI20066820	0	32.943	67.057
	NT2RI20067030	0	59.577	40.423
	NT2RI20074980	0	6.002	24.433
	NT2RI20075890	0	12.002	8.144
	NT2RI20078840	0	22.336	7.578
25	NT2RI20084810	0	12.646	12.87
	NT2RI20089420	0	17.837	18.153
	NT2RP70002380	0	44.979	15.259
	NT2RP70023790	0	2.283	1.549
30	NT2RP70029820	0	15.713	10.661
	NT2RP70049150	0	59.577	40.423
	NT2RP70055020	0	4.911	3.332
	NT2RP70065270	0	1.664	1.129
	NT2RP70069860	0	10.864	7.371
35	NT2RP70075370	0	7.229	1.635
	NT2RP70079750	0	3.104	2.106
	NT2RP70092590	0	17.381	11.793
	OCBBF20000130	0	7.346	19.936
40	PLACE60043970	0	12.827	4.352
	TEST120053960	0	24.609	5.566
	BNGH420004740	0	2.789	0
	HSYRA20002480	0	2.789	0
45	NT2NE10000730	0	24.483	0
	NT2NE20000560	0	4.458	0
	NT2NE20003270	0	28.131	0
	NT2NE20008090	0	34.048	0
	NT2NE20014030	0	17.216	0
50	NT2RP60000720	0	5.865	0
	NT2RP60001090	0	3.47	0
	NT2RP70004770	0	22.083	0
	NT2RP70010800	0	59.331	0
	NT2RP70011660	0	5.472	0
55	NT2RP70028750	0	7.823	0
	NT2RP70029060	0	3.063	0
	NT2RP70030550	0	49.305	0
	NT2RP70032030	0	8.843	0

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Table 4 (continued)

Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
NT2RP70036320	0	8.861	0	9.111
5 NT2RP70064900	0	32.803	0	33.727
NT2RP70093220	0	32.957	0	33.885
NT2RP70093730	0	29.95	0	30.794
SYNOV20013740	0	11.184	0	11.499
10 TEST 120021490	0	20.062	0	6.876
TRACH20004720	0	5.169	0	2.657
TRACH20007800	0	11.333	0	11.652
3NB6920003300	0	0	0.71	1.076
BRACE10000200	0	0	18.865	28.588
15 BRACE20018550	0	0	16.357	12.393
FEBRA20008740	0	0	2.493	3.778
FEBRA20074580	0	0	23.056	34.938
FEBRA20076220	0	0	6.122	2.319
KIDNE20073520	0	0	4.038	3.06
20 MAMGL10000320	0	0	0.39	0.591
NT2NE20002140	0	0	7.614	11.538
NT2NE20006360	0	0	18.047	54.696
NT2NE20007870	0	0	3.883	11.767
25 NT2NE20009800	0	0	39.756	60.244
NT2NE20035690	0	0	14.209	10.766
NT2RI20002940	0	0	12.546	19.012
NT2RI20014500	0	0	3.454	5.235
NT2RI20016210	0	0	21.272	16.117
30 NT2RI20029260	0	0	18.069	54.761
NT2RI20037510	0	0	3.361	5.094
NT2RI20055640	0	0	19.702	29.855
NT2RI20064120	0	0	2.899	4.393
35 NT2RI20074390	0	0	39.756	60.244
NT2RI20077230	0	0	14.643	11.094
NT2RI20090660	0	0	5.676	17.202
PLACE60040050	0	0	3.883	11.767
TRACH20012890	0	0	4.991	2.218
40 3NB6910001730	0	0	0	2.934
BRAGE10001150	0	0	0	1.941
BRACE20011170	0	0	0	3.434
BRACE20020910	0	0	0	19.866
BRACE20035270	0	0	0	8.935
45 BRAWH20005220	0	0	0	12.892
FEBRA20003970	0	0	0	36.013
FEBRA20012450	0	0	0	13.643
HLUNG20003140	0	0	0	13.547
50 IMR3220009350	0	0	0	4.198
IMR3220013170	0	0	0	4.4
IMR3220013320	0	0	0	2.646
IMR3220014350	0	0	0	4.254
NT2NE10000040	0	0	0	49.427
55 NT2NE10000140	0	0	0	100
NT2NE10000180	0	0	0	9.321
NT2NE10000230	0	0	0	100

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Table 4 (continued)

Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
5	NT2NE10000630	0	0	100
	NT2NE10000830	0	0	100
	NT2NE10001200	0	0	100
	NT2NE10001630	0	0	100
	NT2NE10001850	0	0	60.858
10	NT2NE20000380	0	0	64.993
	NT2NE20000640	0	0	100
	NT2NE20001740	0	0	11.757
	NT2NE20002590	0	0	30.217
	NT2NE20002990	0	0	100
15	NT2NE20003690	0	0	100
	NT2NE20003840	0	0	3.017
	NT2NE20003920	0	0	9.486
	NT2NE20004550	0	0	100
20	NT2NE20004700	0	0	33.507
	NT2NE20005170	0	0	61.289
	NT2NE20005360	0	0	100
	NT2NE20005500	0	0	100
	NT2NE20005860	0	0	100
25	NT2NE20006580	0	0	100
	NT2NE20007060	0	0	100
	NT2NE20007630	0	0	15.634
	NT2NE20008020	0	0	100
30	NT2NE20011560	0	0	40.371
	NT2NE20012470	0	0	100
	NT2NE20013240	0	0	100
	NT2NE20013370	0	0	100
	NT2NE20013640	0	0	49.334
35	NT2NE20013720	0	0	100
	NT2NE20014280	0	0	100
	NT2NE20014350	0	0	7.004
	NT2NE20015300	0	0	22.636
40	NT2NE20016230	0	0	100
	NT2NE20016260	0	0	100
	NT2NE20016340	0	0	100
	NT2NE20016480	0	0	100
	NT2NE20016660	0	0	100
45	NT2NE20016970	0	0	61.289
	NT2NE20034080	0	0	100
	NT2NE20044900	0	0	100
	NT2NE20047160	0	0	43
	NT2NE20054410	0	0	34.749
50	NT2NE20055170	0	0	100
	NT2NE20057200	0	0	71.845
	OCBBF20009040	0	0	38.34
	OCBBF20015860	0	0	24.825
55	PLACE60020840	0	0	8.288
	PROST10005260	0	0	11.86
	SKMUS20008630	0	0	2.785
	SMINT20003960	0	0	1.689

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Table 4 (continued)

Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
5	STOMA20001210	0	0	2.199
	SYNOV20011440	0	0	4.179
	TEST110000230	0	0	4.142
	TEST120009700	0	0	15.218
	TEST120040310	0	0	5.364
10	THYMU10003290	0	0	34.388
	TRACH20013950	0	0	12.004
	BGGH120010970	0	2.974	0
	BNGH410001980	0	20.55	0
	BRACE10001660	0	11.3	0
15	BRACE20014770	0	8.968	0
	BRACE20034490	0	6.108	0
	BRACE20071740	0	27.924	0
	BRAWH20009440	0	11.189	0
	BRAWH20036930	0	19.379	0
20	CTONG20020730	0	25.686	0
	CTONG20028030	0	26.479	0
	FCBBF10006750	0	26.462	0
	FCBBF20012110	0	19.363	0
25	FCBBF20015380	0	3.168	0
	FEBRA20007570	0	1.649	0
	FEBRA20043250	0	8.353	0
	FEBRA20068730	0	6.35	0
30	HCASM10001150	0	1.43	0
	HCASM20002140	0	2.71	0
	HHDPC20000950	0	4.733	0
	HHDPC20004620	0	25.354	0
	HSYRA10001370	0	10.795	0
35	HSYRA10001780	0	7.211	0
	HSYRA20001350	0	7.505	0
	HSYRA20006050	0	17.911	0
	IMR3210001580	0	5.369	0
	IMR3220002230	0	4.566	0
40	IMR3220003020	0	4.387	0
	KIDNE20004030	0	3.815	0
	KIDNE20060300	0	1.994	0
	KIDNE20073280	0	6.225	0
45	MESAN20005010	0	24.967	0
	NT2RI10000160	0	100	0
	NT2RI10000270	0	38.568	0
	NT2RI10000480	0	55.06	0
	NT2RI10001640	0	100	0
50	NT2RI20002700	0	100	0
	NT2RI20002820	0	100	0
	NT2RI20003410	0	100	0
	NT2RI20004120	0	15.349	0
55	NT2RI20005970	0	100	0
	NT2RI20006690	0	6.222	0
	NT2RI20006850	0	29.216	0
	NT2RI20007380	0	100	0

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Table 4 (continued)

Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
NT2RI20008650	0	0	100	0
NT2RI20010100	0	0	55.06	0
NT2RI20010830	0	0	100	0
NT2RI20010910	0	0	9.758	0
NT2RI20012350	0	0	100	0
NT2RI20012440	0	0	100	0
NT2RI20014090	0	0	23.941	0
NT2RI20015190	0	0	100	0
NT2RI20015400	0	0	0.383	0
NT2RI20016570	0	0	1.461	0
NT2RI20017260	0	0	73.33	0
NT2RI20018460	0	0	14.383	0
NT2RI20018660	0	0	50.642	0
NT2RI20020220	0	0	39.883	0
NT2RI20020410	0	0	100	0
NT2RI20021520	0	0	14.03	0
NT2RI20022430	0	0	22.43	0
NT2RI20022700	0	0	100	0
NT2RI20025300	0	0	25.585	0
NT2RI20025850	0	0	25.193	0
NT2RI20026540	0	0	5.201	0
NT2RI20028020	0	0	39.201	0
NT2RI20028520	0	0	62.741	0
NT2RI20029580	0	0	8.861	0
NT2RI20029700	0	0	100	0
NT2RI20030110	0	0	2.725	0
NT2RI20030190	0	0	28.31	0
NT2RI20030670	0	0	100	0
NT2RI20031540	0	0	100	0
NT2RI20032050	0	0	100	0
NT2RI20032220	0	0	100	0
NT2RI20033010	0	0	17.133	0
NT2RI20033380	0	0	6.678	0
NT2RI20033440	0	0	31.421	0
NT2RI20033830	0	0	21.125	0
NT2RI20036780	0	0	100	0
NT2RI20041900	0	0	100	0
NT2RI20042840	0	0	21.943	0
NT2RI20043040	0	0	28.031	0
NT2RI20043980	0	0	16.393	0
NT2RI20044420	0	0	100	0
NT2RI20047830	0	0	100	0
NT2RI20048400	0	0	100	0
NT2RI20049160	0	0	100	0
NT2RI20049840	0	0	51.095	0
NT2RI20049850	0	0	17.16	0
NT2RI20050610	0	0	34.993	0
NT2RI20050870	0	0	100	0
NT2RI20056280	0	0	100	0
NT2RI20056470	0	0	0.508	0

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Table 4 (continued)

Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
5	NT2R120058110	0	12.655	0
	NT2R120060710	0	18.232	0
	NT2R120060720	0	36.029	0
	NT2R120061270	0	100	0
	NT2R120061830	0	32.269	0
10	NT2R120062100	0	4.387	0
	NT2R120063450	0	100	0
	NT2R120064870	0	100	0
	NT2R120065060	0	56.418	0
	NT2R120065530	0	2.339	0
15	NT2R120066670	0	100	0
	NT2R120066790	0	100	0
	NT2R120067350	0	28.093	0
	NT2R120067880	0	100	0
	NT2R120068250	0	39.94	0
20	NT2R120068550	0	34.304	0
	NT2R120070480	0	100	0
	NT2R120070840	0	5.538	0
	NT2R120070960	0	39.827	0
25	NT2R120071160	0	100	0
	NT2R120071480	0	8.058	0
	NT2R120072140	0	100	0
	NT2R120072540	0	21.715	0
30	NT2R120073030	0	100	0
	NT2R120073840	0	57.89	0
	NT2R120073860	0	100	0
	NT2R120074690	0	100	0
	NT2R120075070	0	100	0
35	NT2R120077290	0	100	0
	NT2R120077510	0	100	0
	NT2R120077540	0	39.213	0
	NT2R120078270	0	39.208	0
40	NT2R120078790	0	9.741	0
	NT2R120078910	0	100	0
	NT2R120080500	0	100	0
	NT2R120081880	0	100	0
	NT2R120082210	0	2.823	0
45	NT2R120083360	0	5.348	0
	NT2R120085260	0	3.491	0
	NT2R120085980	0	2.71	0
	NT2R120086560	0	13.947	0
	NT2R120087140	0	50.642	0
50	NT2R120087490	0	1.932	0
	NT2R120088010	0	100	0
	NT2R120088120	0	15.273	0
	NT2R120090830	0	24.964	0
55	NT2R120091440	0	100	0
	NT2R120092150	0	100	0
	NT2R120092890	0	100	0
	NTONG10001820	0	8.461	0

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Table 4 (continued)

Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
5	OGBBF20002770	0	39.883	0
	OCBBF20011240	0	7.83	0
	PEBLM10001440	0	18.541	0
	PLACE50001130	0	16.492	0
	PLACE60014430	0	3.227	0
10	PROST20029600	0	40.276	0
	PUAEN10000570	0	8.916	0
	SALGL10001570	0	1.34	0
	SKMUS10000220	0	3.288	0
	SKMUS20004670	0	25.34	0
15	STOMA20002890	0	1.705	0
	SYNOV10001280	0	4.538	0
	TEST120012690	0	3.275	0
	TEST120023690	0	44.022	0
	TEST120028660	0	10.313	0
20	TEST120068720	0	21.478	0
	THYMU10000020	0	27.219	0
	THYMU10000830	0	8.95	0
	TRACH20002370	0	13.11	0
25	3NB6910001290	0	9.099	0
	BRACE10000700	0	22.972	0
	BRACE20003320	0	14.937	0
	BRACE20015080	0	26.275	0
	BRACE20079020	0	59.759	0
30	BRACE20083800	0	4.248	0
	BRACE20092740	0	42.609	0
	FEBRA20000810	0	9.264	0
	FEBRA20017150	0	30.227	0
35	FEBRA20067930	0	58.409	0
	HHDPC20000550	0	14.432	0
	HSYRA20008280	0	7.137	0
	HSYRA20014760	0	5.313	0
40	KIDNE10001450	0	19.263	0
	KIDNE20000850	0	4.841	0
	KIDNE20002660	0	7.078	0
	KIDNE20003300	0	20.763	0
	KIDNE20033050	0	1.709	0
45	KIDNE20045340	0	17.723	0
	NT2RP60000080	0	100	0
	NT2RP60000170	0	100	0
	NT2RP60000320	0	100	0
	NT2RP60000390	0	100	0
50	NT2RP60000590	0	100	0
	NT2RP60000860	0	100	0
	NT2RP60001000	0	100	0
	NT2RP60001230	0	5.146	0
55	NT2RP60001270	0	100	0
	NT2RP70000410	0	100	0
	NT2RP70000690	0	66.955	0
	NT2RP70002590	0	31.56	0

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Table 4 (continued)

	Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
	NT2RP70002710	0	14.558	0	0
5	NT2RP70003640	0	100	0	0
	NT2RP70003910	0	100	0	0
	NT2RP70004250	0	100	0	0
	NT2RP70005790	0	100	0	0
10	NT2RP70006240	0	100	0	0
	NT2RP70008120	0	100	0	0
	NT2RP70009060	0	8.617	0	0
	NT2RP70012310	0	24.404	0	0
	NT2RP70013060	0	49.874	0	0
15	NT2RP70013350	0	30.221	0	0
	NT2RP70015910	0	22.4	0	0
	NT2RP70018560	0	100	0	0
	NT2RP70021510	0	49.439	0	0
20	NT2RP70022430	0	33.36	0	0
	NT2RP70023760	0	17.87	0	0
	NT2RP70024490	0	22.701	0	0
	NT2RP70024500	0	19.57	0	0
	NT2RP70025540	0	100	0	0
25	NT2RP70026190	0	9.482	0	0
	NT2RP70028290	0	49.972	0	0
	NT2RP70028410	0	100	0	0
	NT2RP70030500	0	100	0	0
30	NT2RP70030910	0	20.809	0	0
	NT2RP70033040	0	100	0	0
	NT2RP70036290	0	9.965	0	0
	NT2RP70036470	0	24.999	0	0
	NT2RP70039600	0	15.306	0	0
35	NT2RP70040800	0	100	0	0
	NT2RP70042040	0	9.773	0	0
	NT2RP70042330	0	60.574	0	0
	NT2RP70042600	0	71.279	0	0
40	NT2RP70043730	0	7.505	0	0
	NT2RP70043960	0	100	0	0
	NT2RP70045410	0	24.679	0	0
	NT2RP70046560	0	100	0	0
	NT2RP70046870	0	100	0	0
45	NT2RP70047510	0	100	0	0
	NT2RP70047660	0	100	0	0
	NT2RP70047900	0	18.549	0	0
	NT2RP70049250	0	27.784	0	0
	NT2RP70049750	0	100	0	0
50	NT2RP70052050	0	64.358	0	0
	NT2RP70052190	0	100	0	0
	NT2RP70054680	0	100	0	0
	NT2RP70054930	0	49.38	0	0
55	NT2RP70055130	0	3.248	0	0
	NT2RP70055200	0	19.133	0	0
	NT2RP70061620	0	100	0	0
	NT2RP70061880	0	20.642	0	0

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Table 4 (continued)

Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
5	NT2RP70062960	0	100	0
	NT2RP70063040	0	100	0
	NT2RP70063740	0	100	0
	NT2RP70064080	0	100	0
	NT2RP70066210	0	100	0
10	NT2RP70067010	0	100	0
	NT2RP70069800	0	40.229	0
	NT2RP70071140	0	33.145	0
	NT2RP70071540	0	49.972	0
	NT2RP70072210	0	100	0
15	NT2RP70072520	0	100	0
	NT2RP70073590	0	100	0
	NT2RP70073810	0	100	0
	NT2RP70074060	0	100	0
	NT2RP70075040	0	100	0
20	NT2RP70076100	0	36.014	0
	NT2RP70076170	0	100	0
	NT2RP70076430	0	100	0
	NT2RP70079250	0	100	0
25	NT2RP70079300	0	71.279	0
	NT2RP70081330	0	100	0
	NT2RP70081370	0	26.129	0
	NT2RP70081420	0	100	0
30	NT2RP70081440	0	100	0
	NT2RP70081670	0	100	0
	NT2RP70083150	0	100	0
	NT2RP70084060	0	100	0
	NT2RP70084410	0	65.611	0
35	NT2RP70084870	0	48.444	0
	NT2RP70085500	0	100	0
	NT2RP70085570	0	9.069	0
	NT2RP70086230	0	100	0
	NT2RP70087200	0	100	0
40	NT2RP70088550	0	15.625	0
	NT2RP70090120	0	49.497	0
	NT2RP70090190	0	100	0
	NT2RP70091490	0	49.38	0
45	NT2RP70091680	0	100	0
	NT2RP70092150	0	100	0
	NT2RP70092360	0	100	0
	NT2RP70093630	0	100	0
	NT2RP70093700	0	100	0
50	NT2RP70093940	0	24.073	0
	NT2RP70093970	0	100	0
	NT2RP70094290	0	100	0
	NT2RP70094660	0	100	0
55	NT2RP70094810	0	58.409	0
	NT2RP70094980	0	44.133	0
	NT2RP70095020	0	100	0
	NT2RP70095070	0	100	0

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Table 4 (continued)

Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
NTONG10000980	0	10.097	0	0
NTONG10002140	0	12.777	0	0
NTONG20002650	0	10.048	0	0
NTONG20016120	0	21.562	0	0
PEBLM20003950	0	8.711	0	0
PROST10005640	0	10.708	0	0
PROST20003250	0	24.163	0	0
SKNMC20000650	0	3.384	0	0
SKNSH10000860	0	23.605	0	0
SKNSH20003470	0	15.832	0	0
TEST110000510	0	11.33	0	0
TEST110000960	0	51.106	0	0
TEST120015110	0	65.524	0	0
TEST120074640	0	12.147	0	0
TRACH20004610	0	13.344	0	0

Table 5

Clone ID	BEAST	TBAES
3NB6910001730	0	33.793
FCBBF10007600	0	75.606
KIDNE20033050	0	40.478
KIDNE20060300	0	69.585
NT2R120065530	0	81.65
NT2RP60000720	0	69.448
NT2RP70075370	0	57.062
TRACH20004200	0	94.946
LIVER10000670	68.212	0
LIVER10005420	78.818	0
LIVER20000370	73.799	0

Table 6

Clone ID	CERVX	TCERX
BRACE10001590	0	57.778
HHDFC20000950	0	40.177
HSYRA20016210	0	10.84
NT2R120074980	0	46.086
3NB6920014330	69.325	0
NT2R120087490	33.161	0
NT2RP60001090	80.827	0
PROST10002200	42.592	0
SKNMC20003220	58.42	0
STOMA20001210	49.81	0

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Table 7

Clone ID	COLON	TCOLN
BFACE20028610	0	95.142
BFACE20011170	78.541	0
BFACE20035940	95.04	0
IMR3220013320	60.529	0
NT2NE20053710	26.798	0

Table 8

Clone ID	NESOP	TESOP
KIDNE20005740	0	54.924
MAMGL10000320	0	13.581
NESOP10000870	49.196	0
NT2R120056470	69.766	0
NTONG20008000	78.683	0

Table 9

Clone ID	KIDNE	TKIDN
3NB6920002810	0	1.507
ADRGL10000020	0	12.08
BNGH420004740	0	3.392
BFACE10000200	0	33.823
BFACE10000420	0	4.476
BFACE10000730	0	35.7
BFACE10001590	0	3.051
BFACE20005650	0	55.211
BFACE20016730	0	41.8
BFACE20028120	0	21.571
BFACE20077980	0	4.39
BFACE20083800	0	15.501
BFACE20083850	0	25.281
BRAWH10001740	0	23
BRAWH20036930	0	11.581
BRAWH20064500	0	14.412
BRAWH20064930	0	40.792
CTONG20028030	0	15.825
FCBBF20015380	0	17.038
FEBRA20005360	0	7.956
FEBRA20007570	0	2.956
FEBRA20008740	0	4.47
FEBRA20012270	0	24.184
FEBRA20025250	0	20.688
HSYRA20002480	0	3.392
HSYRA20006400	0	4.833
HSYRA20008280	0	2.894
HSYRA20015740	0	9.842
HSYRA20016210	0	2.862
IMR3220009350	0	4.967
LIVER10001110	0	25.88

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Table 9 (continued)

	Clone ID	KIDNE	TKIDN
	NT2NE20003920	0	3.741
5	NT2NE20007630	0	18.497
	NT2NE20007870	0	6.961
	NT2RI20025410	0	21.344
	NT2RI20026540	0	4.662
10	NT2RI20029580	0	15.887
	NT2RI20033380	0	23.947
	NT2RI20033830	0	12.625
	NT2RI20051500	0	4.126
	NT2RI20058110	0	7.563
15	NT2RI20090650	0	3.609
	NT2RP60000720	0	3.567
	NT2RP70013350	0	9.191
	NT2RP70023790	0	2.777
20	NT2RP70024490	0	27.614
	NT2RP70028750	0	3.807
	NT2RP70029060	0	11.18
	NT2RP70036800	0	7.976
	NT2RP70075370	0	2.931
25	NT2RP70076100	0	14.603
	NTONG10000980	0	8.189
	NTONG10002460	0	4.695
	NTONG20015500	0	30.566
30	OCBBF20002310	0	20.844
	OCBBF20013070	0	18.625
	PEBLM20001470	0	8.936
	PEBLM20003950	0	5.298
	PLACE60021510	0	12.663
35	PLACE60040050	0	6.961
	PLACE60043970	0	7.802
	PROST20051430	0	37.542
	STOMA20001210	0	2.602
	STOMA20002570	0	14.983
40	STOMA20002890	0	1.528
	SYNOV20011440	0	4.944
	TESTI10000230	0	4.9
	TESTI20009700	0	18.005
45	TESTI20021490	0	8.135
	TESTI20032800	0	21.55
	TESTI20053960	0	9.979
	TESTI20080200	0	1.673
	TESTI20082400	0	2.876
50	BGGI120010970	4.336	0
	BRACE20004210	3.583	0
	BRACE20005250	6.242	23.03
	BRACE20011170	3.303	0
	BRACE20020910	19.111	0
55	BRACE20080970	20.33	0
	BRAWH20000340	10.476	0
	BRAWH20006970	3.96	0

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Table 9 (continued)

	Clone ID	KIDNE	TKIDN
5	BRAW120011660	5.897	0
	FCBBF20001950	65.363	0
	FEBRA20043250	12.177	0
	HLUNG10000640	23.921	0
	IMR3220007420	2.375	0
10	IMR3220014350	4.092	0
	KIDNE10000080	22.13	0
	KIDNE10000280	100	0
	KIDNE10000500	15.868	0
	KIDNE10001040	100	0
15	KIDNE10001430	100	0
	KIDNE10001450	19.052	0
	KIDNE10001520	100	0
	KIDNE20000410	100	0
	KIDNE20000510	100	0
20	KIDNE20000700	100	0
	KIDNE20000850	4.788	0
	KIDNE20001670	100	0
	KIDNE20001920	100	0
	KIDNE20002440	37.565	0
25	KIDNE20002450	100	0
	KIDNE20002660	7	0
	KIDNE20003150	100	0
	KIDNE20003300	20.536	0
	KIDNE20003490	64.026	5.625
30	KIDNE20003750	100	0
	KIDNE20004030	5.561	0
	KIDNE20004220	35.77	0
	KIDNE20004970	12.49	0
	KIDNE20005130	100	0
35	KIDNE20005170	81.524	0
	KIDNE20005190	100	0
	KIDNE20005740	2.3	0
	KIDNE20031850	16.193	0
	KIDNE20033050	3.381	0
40	KIDNE20033350	100	0
	KIDNE20033570	53.825	0
	KIDNE20033730	100	0
	KIDNE20033770	100	0
	KIDNE20037520	100	0
45	KIDNE20039410	100	0
	KIDNE20039940	43.968	0
	KIDNE20040340	100	0
	KIDNE20040540	49.114	0
	KIDNE20040840	100	0
50	KIDNE20042620	100	0
	KIDNE20042940	100	0
	KIDNE20042950	100	0
	KIDNE20043440	100	0
	KIDNE20044110	7.51	0

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Table 9 (continued)

Clone ID	KIDNE	TKIDN
KIDNE20045200	100	0
5 KIDNE20045340	17.53	0
KIDNE20045790	100	0
KIDNE20046810	100	0
KIDNE20048280	100	0
10 KIDNE20048640	34.264	0
KIDNE20048790	100	0
KIDNE20049810	100	0
KIDNE20050420	35.626	0
KIDNE20052960	100	0
15 KIDNE20053360	58.142	0
KIDNE20054000	49.697	0
KIDNE20054770	100	0
KIDNE20056290	100	0
20 KIDNE20056760	16.262	0
KIDNE20059080	100	0
KIDNE20059370	88.03	0
KIDNE20060140	13.852	0
KIDNE20060300	2.906	0
25 KIDNE20060530	100	0
KIDNE20060620	100	0
KIDNE20061490	100	0
KIDNE20062990	31.685	0
30 KIDNE20063530	26.747	0
KIDNE20063760	100	0
KIDNE20066520	70.185	0
KIDNE20067600	100	0
KIDNE20067750	8.487	0
35 KIDNE20068800	24.137	0
KIDNE20070050	66.711	0
KIDNE20070770	100	0
KIDNE20071860	39.822	0
KIDNE20073280	4.537	0
40 KIDNE20073520	8.83	3.62
KIDNE20073560	100	0
KIDNE20074220	100	0
KIDNE20075690	100	0
45 KIDNE20078100	100	0
KIDNE20078110	100	0
LIVER10000790	15.673	0
MAMGL10000320	1.138	0
NB9N410000470	3.598	0
50 NT2NE20053710	1.127	0
NT2RI20006710	2.454	0
NT2RI20013420	2.015	0
NT2RI20016570	23.435	0
55 NT2RI20018460	20.967	0
NT2RI20025540	5.573	0
NT2RI20040590	13.676	0
NT2RI20065530	3.41	0

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Table 9 (continued)

	Clone ID	KIDNE	TKIDN
5	NT2R120087490	1.408	0
	NT2R120087910	2.824	0
	NT2RP60000350	5.311	0
	NT2RP60001230	5.09	0
	NT2RP70043730	14.846	0
10	NT2RP70069860	10.745	26.431
	NT2RP70074220	3.96	0
	OCBBF20014940	49.164	0
	PLACE60020840	2.658	0
	PLACE60043120	3.992	9.82
15	PROST10003430	25.547	0
	SKNSH20001510	20.208	0
	SMINT10000160	38.817	15.914
	SPLN20000	66.711	0
	SPLN20001340	88.909	0
20	SPLN20003570	31.635	0
	STOMA10000470	17.849	0
	TEST110000700	25.214	0
	TEST120027070	14.795	0
	TEST120040310	2.58	0
25	TRACH10000300	11.119	0
	TRACH20000790	4.534	11.153
	TRACH20002500	35.282	0
	TRACH20007800	5.605	0
30			

Table 10

	Clone ID	LIVER	TLIVE
35	FCBBF50002610	0	88.758
	FEBRA20076220	0	53.946
	KIDNE20033050	0	40.878
	NT2NE20003840	0	70.165
	KIDNE20062480	7.391	0
40	KIDNE20068800	60.015	0
	LIVER10000580	100	0
	LIVER10000670	31.788	0
	LIVER10000790	77.941	0
	LIVER10000990	100	0
45	LIVER10001040	100	0
	LIVER10001110	52.319	0
	LIVER10001750	100	0
	LIVER10002300	66.114	0
	LIVER10002780	100	0
50	LIVER10003030	100	0
	LIVER10004330	100	0
	LIVER10005420	13.604	0
	LIVER20000330	100	0
	LIVER20004160	33.27	0
55	LIVER20004460	100	0

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Table 10 (continued)

Clone ID	LIVER	TLIVE
LIVER20005150	100	0
NT2NE20002140	27.596	0
NT2RI20030510	18.459	0
NT2RI20043040	50.8	0
NT2RI20090650	7.296	0
PROST10005640	26.335	0
PROST20032320	15.404	0
SALGL10001570	2.428	0
SMINT10000160	32.172	0
SPLEN20002420	83.286	0
TESTI20002530	26.418	0
TESTI20080200	3.383	0
THYMU10003590	7.302	0
TRACH20004720	6.356	0

Table 11

Clone ID	HLUNG	TLUNG
NT2RI20030110	0	94.571
BNGH410001980	16.113	0
BRACE10000420	7.831	0
BRACE10001150	1.339	0
BRACE20014770	28.126	0
BRACE20018550	25.65	0
BRAWH20006970	8.521	0
BRAWH20014610	7.03	77.801
FEBRA20008810	19.713	0
FEBRA20015840	53.019	0
FEBRA20044120	15.75	0
HHDPC20001490	25.611	0
HLUNG10000240	100	0
HLUNG10000300	100	0
HLUNG10000370	100	0
HLUNG10000640	51.466	0
HLUNG10000760	12.838	0
HLUNG10000990	100	0
HLUNG10001050	100	0
HLUNG10001100	100	0
HLUNG20000680	72.532	0
HLUNG20001160	100	0
HLUNG20001250	100	0
HLUNG20001420	79.349	0
HLUNG20001760	100	0
HLUNG20002550	100	0
HLUNG20003140	14.018	0
HLUNG20004120	42.131	0
HLUNG20004800	100	0
HLUNG20005010	5.302	0
HSYRA20014	12.578	0

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Table 11 (continued)

Clone ID	HLUNG	TLUNG
KIDNE20002660	15.061	0
KIDNE20033050	3.637	0
NT2NE20014350	28.99	0
NT2RI20016570	9.167	0
NT2RI20026540	8.156	0
NT2RI20051500	21.652	0
NT2RI20064120	9.093	0
NT2RI20083960	17.851	0
NT2RI20085260	5.474	0
NT2RI20087490	3.03	0
NT2RP7009060	18.337	0
NT2RP70011660	5.822	0
NT2RP70029060	6.519	0
NT2RP70055020	10.451	0
NT2RP70074220	8.521	0
NT2RP70076100	25.546	0
NTONG10002460	16.426	0
NTONG20008000	7.189	0
PLACE60043120	8.589	0
SKMUS20016340	15.317	0
SKNMC20005930	13.727	0
SMINT20000180	38.989	0
SMINT20002390	51.283	0
SMINT20002770	12.776	0
SMINT20003960	10.489	0
STOMA10000470	38.402	0
STOMA20001880	52.43	0
SYNOV2001374	23.798	0
TEST120036250	32.684	0
TEST120080200	2.927	0
TRACH20004610	28.395	0

Table 12

Clone ID	NOVAR	TOVAR
BRACE20011880	0	93.107
TEST120030710	0	79.631
BRACE20076210	97.13	0
NT2RI20053680	78.467	0
SKMUS20008630	61.727	0
TEST120005910	94.963	0
TEST120040310	59.442	0

Table 13

Clone ID	STOMA	TSTOM
HSYRA20011030	0	60.206
NT2RI20013420	0	48.779
NT2RP70079750	0	74.336

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Table 13 (continued)

Clone ID	STOMA	TSTOM
BRACE20003320	28.838	0
HEART20005060	8.996	0
HHDPC20000950	3.367	0
HLUNG20004120	38.225	0
HLUNG20005010	4.81	0
HSYRA20006400	23.013	0
KIDNE10000500	30.974	0
KIDNE20062480	2.901	0
NT2NE20053710	2.2	0
NT2NE20054410	65.251	0
NT2RI20015400	0.544	0
NT2RI20016570	4.159	0
NT2RI20064120	8.25	0
NT2RI20070840	15.758	0
NT2RI20071330	13.128	0
NT2RI20074980	3.862	0
NT2RI20077230	20.833	0
NT2RI20089420	17.218	0
NT2RP70000760	4.442	0
NT2RP70028750	3.021	0
PLACE60014430	9.182	0
PLACE60024190	54.046	0
SKNMC20000970	4.463	0
STOMA10000470	34.842	0
STOMA10000520	100	0
STOMA10001170	100	0
STOMA10001330	100	0
STOMA10001860	100	0
STOMA20000320	100	0
STOMA20000880	100	0
STOMA20001210	4.129	0
STOMA20001880	47.57	0
STOMA20002570	23.78	0
STOMA20002890	4.851	0
STOMA20003960	100	0
STOMA20004780	100	0
STOMA20004820	28.859	0
THYMU10003590	5.733	0

Table 14

Clone ID	UTERU	TUTER
NT2R120085260	0	60.829
3NB6920002810	1.339	0
BRACE10000420	15.908	0
BRACE20089990	28.795	0
BRACE20092120	61.611	0
BRAWH10001680	49.225	0
BRAWH20011410	14.576	0

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Table 14 (continued)

Clone ID	UTERU	TUTER
BRAWH20011660	3.222	0
FCBBF20005910	17.567	0
FCBBF50002610	4.011	0
FEBRA20005360	7.069	0
FEBRA20006800	81.993	0
FEBRA20008800	29.932	0
FEBRA20044120	7.999	0
FEBRA20057520	14.823	0
HEART20005060	5.036	0
HHGPC20000950	1.885	0
HLUNG10000760	3.26	0
HLUNG20003140	7.12	0
HSYRA20014200	6.388	0
HSYRA20014760	5.742	0
HSYRA20015800	36.126	0
IMR3210002420	7.465	0
IMR3220002230	3.637	0
IMR3220009350	4.412	0
IMR3220014350	4.472	0
IMR3220016000	0.788	0
KIDNE20000850	5.232	0
KIDNE20060140	15.135	0
KIDNE20060300	3.176	0
MAMGL10000350	1.122	0
NT2NE20035690	11.316	0
NT2NE20053710	1.232	0
NT2R110000270	61.432	0
NT2R120000640	3.308	0
NT2R120002940	19.984	0
NT2R120010910	15.542	0
NT2R120013420	2.201	0
NT2R120016570	2.328	0
NT2R120033380	10.637	0
NT2R120036950	5.07	0
NT2R120037510	2.677	0
NT2R120053350	2.517	0
NT2R120057230	2.613	0
NT2R120058110	6.719	0
NT2R120071480	25.67	0
NT2R120074980	4.324	0
NT2R120084810	20.5	0
NT2R120087490	1.539	0
NT2R120087910	12.345	0
NT2RP60000350	1.451	0
NT2RP70032030	4.778	0
NT2RP70043730	8.111	0
NTONG10000980	7.275	0
NTONG10002460	4.171	0
PLACE60014430	10.28	0
PLACE60026680	15.19	0

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Table 14 (continued)

Clone ID	UTERU	TUTER
PLACE60043960	10.84	0
PLACE60044910	52.136	0
PLACE60047380	52.136	0
PROST10002200	1.976	0
PROST10005260	12.466	0
PROST20025910	51.788	0
PROST20033380	16.15	0
PUAEN10000570	14.201	0
SALGL10001570	1.067	0
SKMUS10000140	23.507	0
SKMUS20003430	35.091	0
SKMUS20009540	9.414	0
SKNMC10002510	6.618	0
SKNMC20000970	2.498	0
SKNSH10000860	25.511	0
SMINT20002770	3.244	0
STOMA20002890	2.716	0
SYNOV20011440	4.393	0
TESTI10000230	8.707	0
TESTI20018290	12.741	0
TESTI20021490	14.455	0
TESTI20080200	2.973	0
TESTI20082400	2.555	0
TRACH10000300	12.149	0
TRACH20002370	20.883	0
TRACH20007800	12.248	0
TRACH20012890	4.662	0
UTERU10000770	100	0
UTERU10000960	50.58	0
UTERU10001600	100	0
UTERU10001920	100	0
UTERU20000470	100	0
UTERU20003380	35.158	0
UTERU2000039	100	0
UTERU20004850	100	0
UTERU20005410	33.583	0
UTERU20005690	50.58	0

Table 15

Clone ID	NTONG	CTONG
3NB6910001160	0	6.048
3NB6910001290	0	3.009
3NB6910001730	0	0.944
BNGH420004740	0	3.688
BRACE20008850	0	15.357
BRACE20020910	0	12.778
BRACE20074010	0	5.637
BRAWH20014840	0	5.251

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Table 15 (continued)

	Clone ID	NTONG	CTONG
5	BRAW120089560	0	21.778
	CTONG20003030	0	100
	CTONG20005890	0	39.66
	CTONG20007710	0	100
	CTONG20008270	0	18.957
10	CTONG20011390	0	100
	CTONG20013200	0	19.93
	CTONG20013660	0	100
	CTONG20015330	0	100
	CTONG20018200	0	100
15	CTONG20019110	0	48.152
	CTONG20019550	0	100
	CTONG20020730	0	25.035
	CTONG20021430	0	100
	CTONG20024180	0	100
20	CTONG20024530	0	23.734
	CTONG20025580	0	57.263
	CTONG20027210	0	100
	CTONG20028030	0	8.603
	CTONG20028160	0	100
25	CTONG20028200	0	55.786
	CTONG20029650	0	100
	GTONG20037820	0	100
	CTONG20047160	0	100
	CTONG20055530	0	38.023
30	CTONG20064490	0	24.327
	FEBRA20003770	0	22.646
	FEBRA20004520	0	19.228
	FEBRA20007400	0	4.377
	FEBRA20007570	0	1.607
35	FEBRA20012940	0	7.503
	FEBRA20021940	0	1.128
	FEBRA20044120	0	4.895
	HCASM10001150	0	1.394
	HHDP20004560	0	18.986
40	HLUNG20003140	0	4.356
	HSYRA20002480	0	3.688
	IMR3220009350	0	2.7
	IMR3220012180	0	3.684
	KIDNE20000850	0	1.601
45	KIDNE20002660	0	9.361
	KIDNE20004220	0	23.916
	KIDNE20005740	0	1.538
	KIDNE20056760	0	21.746
	KIDNE20060140	0	9.261
50	KIDNE20062480	0	2.981
	MESAN20000920	0	19.727
	MESAN20003370	0	17.82
	NHNP20002060	0	4.429
	NT2NE10001850	0	39.142

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Table 15 (continued)

	Clone ID	NTONG	CTONG
5	NT2NE20000560	0	8.845
	NT2NE20002140	0	7.421
	NT2NE20003270	0	27.905
	NT2NE20003840	0	1.94
10	NT2NE20014350	0	4.505
	NT2NE20053710	0	3.014
	NT2RI20006690	0	12.129
	NT2RI20006710	0	1.64
15	NT2RI20016570	0	1.424
	NT2RI20018660	0	49.358
	NT2R120025300	0	49.872
	NT2R120025410	0	11.603
20	NT2R120030190	0	27.593
	NT2R120030510	0	9.928
	NT2RI20036950	0	6.205
	NT2RI20046060	0	12.778
25	NT2RI20053350	0	4.621
	NT2RI20067350	0	27.381
	NT2R120075720	0	8.573
	NT2RI20078790	0	3.165
30	NT2RI20083960	0	5.548
	NT2RI20087140	0	49.358
	NT2RI20094060	0	8.828
	NT2RP60000350	0	5.327
35	NT2RP60001230	0	6.806
	NT2RP70000760	0	12.173
	NT2RP70004770	0	36.51
	NT2RP70009060	0	5.699
40	NT2RP70011660	0	5.428
	NT2RP70023760	0	11.817
	NT2RP70023790	0	3.02
	NT2RP70024500	0	12.942
45	NT2RP70026190	0	12.541
	NT2RP70029820	0	10.391
	NT2RP70036470	0	33.064
	NT2RP70043730	0	4.963
50	NT2RP70061880	0	27.302
	NT2RP70071770	0	18.778
	NT2RP70076100	0	7.939
	NT2RP70079750	0	4.105
55	NT2RP70084870	0	32.036
	NT2RP70093730	0	19.806
	OCBBF20013070	0	5.063
	PEBLM20003950	0	5.761
	PLACE60037450	0	33.178
	PLACE60043120	0	2.669
	PROST10003	0	34.162
	PROST10005260	0	7.628
	PROST2003232	0	8.285
	PROST2003302	0	6.218

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Table 15 (continued)

	Clone ID	NTONG	CTONG
	PROST20056040	0	29.772
5	SKNMC10002510	0	8.098
	SKNMC20000650	0	4.476
	SKNMC20010570	0	4.712
	SKNSH20003470	0	10.47
10	SMINT20000180	0	24.233
	SYNOV20013740	0	7.396
	TEST110000230	0	7.991
	TEST110001680	0	8.412
	TEST120007840	0	17.514
15	TEST120021490	0	4.422
	TEST120022230	0	62.139
	TEST120023690	0	42.906
	TEST120030050	0	1.535
	TEST120042950	0	76.649
20	TEST120068720	0	10.467
	TEST120080200	0	0.91
	TRACH20012890	0	1.426
	BRACE20006980	55.471	0
25	BRACE20092740	22.273	0
	BRAWH20006970	8.372	0
	FCBBF10007600	6.676	0
	FEBRA20062700	19.42	6.142
30	IMR3220016000	3.049	0.482
	KIDNE20073280	9.592	3.034
	MAMGL10000350	2.171	0
	NT2NE20035690	21.893	0
	NT2RI20056470	23.487	5.448
35	NT2RI20058110	12.999	0
	NT2RI20084810	13.22	0
	NT2RI20085260	5.378	0
	NT2RP70015910	46.836	14.813
40	NT2RP70036290	20.836	59.311
	NT2RP70036320	18.528	46.879
	NT2RP70074220	8.372	0
	NT2RP70075370	5.038	0
	NTONG10000330	100	0
45	NTONG10000520	44.434	0
	NTONG10001230	100	0
	NTONG10001300	100	0
	NTONG10001820	39.112	0
	NTONG10002140	80.147	0
50	NTONG10002460	8.07	0
	NTONG10002570	100	0
	NTONG10002640	67.153	0
	NTONG20002650	21.01	6.645
55	NTONG20003340	27.701	0
	NTONG20003630	100	0
	NTONG20004920	100	0
	NTONG20005830	100	0

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Table 15 (continued)

Clone ID	NTONG	CTONG
NTONG20008000	14.128	0
NTONG20008780	100	0
NTONG20009660	100	0
NTONG20009850	100	0
NTONG20011370	100	0
NTONG20012220	100	0
NTONG20014280	76.302	0
NTONG20015500	52.537	0
NTONG20016120	45.084	0
OCBBF20011240	24.128	0
OCBBF20015860	50.483	0
PROST10002200	22.942	1.209
SKMUS20016340	15.05	4.76
SKNMC20000970	4.833	1.529
STOMA20004820	31.253	9.885
SYNOV10001280	13.986	0
SYNOV20011440	8.499	0
THYMU10000830	27.581	0
TRACH20000790	19.169	0
TRACH20009260	30.323	9.59

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Table 16

Core ID	FCBBF	FERRA	ICBBF	BRICE	BRALZ	BRANV	BRANW	BRANC	BRDOC	BRHIC	BRSNS	BRSIN	BIRTH
BRACE20029960	0	0	0	37.659	0	0	62.941	0	0	0	0	0	0
BRACE20074010	0	0	0	17.222	8.739	16.508	28.509	5.549	8.568	5.733	0	0	0
BRACE20077080	0	0	0	8.944	0	0	14.807	17.29	26.659	0	0	0	0
BRACE20077980	0	0	0	7.291	7.4	2.344	8.046	9.396	3.627	4.854	19.055	18.412	0
BRACE20083800	0	0	0	2.86	8.705	8.275	4.735	11.059	12.807	5.713	4.485	17.335	0
BRACE20088570	0	0	0	24.099	0	0	39.884	0	0	0	0	0	0
BRANH10000070	0	0	0	0	15.441	0	33.582	9.804	15.139	10.129	15.905	0	0
BRANH10000020	0	0	0	0	0	0	100	0	0	0	0	0	0
BRANH10000070	0	0	0	0	0	0	34.097	0	0	0	0	0	0
BRANH10000370	0	0	0	0	0	0	34.637	0	0	0	0	0	0
BRANH10000940	0	0	0	0	0	0	100	0	0	0	0	0	0
BRANH10001300	0	0	0	0	0	0	100	0	0	0	0	0	0
BRANH10001640	0	0	0	0	0	0	100	0	0	0	0	0	0
BRANH10001680	0	0	0	0	0	0	50.775	0	0	0	0	0	0
BRANH10001740	0	0	0	0	0	0	21.077	36.92	19.003	0	0	0	0
BRANH10001800	0	0	0	0	0	0	100	0	0	0	0	0	0
BRANH20000340	0	0	0	0	0	0	11.808	0	10.646	0	0	0	0
BRANH20000340	0	0	0	0	0	0	11.808	0	10.646	0	0	0	0
BRANH20000480	0	0	0	0	0	0	100	0	0	0	0	0	0
BRANH20000930	0	0	0	0	0	0	100	0	0	0	0	0	0
BRANH20001770	0	0	0	0	0	0	11.171	6.522	0	6.739	0	0	0
BRANH20002480	0	0	0	0	0	0	100	0	0	0	0	0	0
BRANH20003230	0	0	0	0	0	0	100	0	0	0	0	0	0
BRANH20004430	0	0	0	0	0	0	100	0	0	0	0	0	0
BRANH20004760	0	0	0	0	0	0	62.374	0	0	37.626	0	0	0
BRANH20005030	0	0	0	0	0	0	32.294	0	0	38.962	0	0	0
BRANH20005540	0	0	0	0	0	0	100	0	0	0	0	0	0
BRANH20006340	0	0	0	0	0	0	3.43	5.888	0	0	0	0	0
BRANH20006510	0	0	0	0	0	0	100	0	0	0	0	0	0
BRANH20006970	0	0	0	0	8.209	0	8.927	2.605	12.073	2.693	8.456	8.171	0
BRANH20008660	0	0	0	0	0	0	100	0	0	0	0	0	0
BRANH20008920	0	0	0	0	0	0	100	0	0	0	0	0	0
BRANH20009010	0	0	0	0	0	0	100	0	0	0	0	0	0
BRANH20009440	0	0	0	0	0	0	18.383	0	0	0	0	0	0
BRANH20009840	0	0	0	0	0	0	100	0	0	0	0	0	0

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Table 18

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Table 34

NTONG10005960	3.528	0	6.884	2.266	0	0	0	3.752	0	0	4.527	3.554	0	0
NTONG20016120	11.301	0	22.052	0	0	0	0	0	0	0	0	0	0	0
OCBBF20011240	12.096	0	11.402	0	0	0	0	0	0	0	0	0	0	0
OCBBF20012100	42.373	0	41.34	0	0	0	0	0	0	0	0	0	0	0
OCBBF20013070	4.012	0	7.829	0	0	9.943	23.082	10.296	16.167	0	0	0	0	0
OCBBF20014020	33.884	0	66.116	0	0	0	0	0	0	0	0	0	0	0
PEBL420003950	9.132	0	4.455	0	0	0	4.855	0	0	0	0	0	0	0
PLACE50001130	12.74	0	24.859	0	0	0	0	0	0	0	0	0	0	0
PLACE60021510	27.281	0	10.846	0	0	0	13.551	0	0	0	0	0	0	0
PULENT10000570	3.444	0	13.439	0	0	0	7.324	4.276	0	0	0	0	0	0
SKMWC20000970	2.423	0	1.182	1.557	0	0	2.577	0	0	0.777	0	0	0	0
TEST1120040310	1.367	0	2.668	0	0	0	0	0	0	0	2.754	0	0	0
TRACH20004610	6.984	0	13.647	0	0	0	0	0	13.411	0	0	0	0	0
3N66220006450	3.772	5.125	0	4.847	0	0	0	0	0	0	0	0	0	0
BRACE10000420	3.858	2.62	0	2.478	3.772	2.39	4.102	2.385	7.397	7.424	0	0	0	0
BRACE20016410	27.661	18.803	0	8.891	13.535	17.149	0	0	0	13.942	0	0	0	0
BRACE20018820	7.658	10.458	0	39.561	0	9.538	32.745	0	0	0	0	0	0	0
BRAMW20006860	6.302	25.883	0	0	0	0	26.805	0	12.084	0	0	12.267	0	0
BRAMW20008030	9.261	12.609	0	0	0	11.5	19.141	23.052	0	23.817	0	0	0	0
FCBBF10006760	20.441	27.77	0	0	0	25.327	0	0	0	0	0	0	0	0
FCBBF10006860	42.399	57.601	0	0	0	0	0	0	0	0	0	0	0	0
FCBBF20015360	7.341	3.324	0	5.288	0	9.095	0	5.078	0	15.698	9.86	4.764	0	0
FCBBF50009610	1.945	5.265	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20004520	45.718	20.704	0	17.618	0	4.247	0	0	0	0	4.398	0	0	0
FEBRA20003560	3.428	9.315	0	0	0	0	0	0	4.257	0	0	0	0	0
FEBRA20009010	23.228	31.556	0	0	0	0	0	0	0	0	0	45.216	0	0
FEBRA20014920	42.399	57.601	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20015840	13.059	17.141	0	0	0	16.18	0	0	0	0	0	0	0	0
FEBRA20021910	10.174	13.622	0	0	0	12.605	0	0	0	0	0	0	0	0
FEBRA20021940	0.894	2.429	0	2.297	3.497	1.108	0	1.11	0	0	0	1.74	0	0
FEBRA20043250	6.453	8.767	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20057780	12.772	34.702	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20057880	22.294	30.288	0	0	0	0	47.417	0	0	0	0	0	0	0
FEBRA20066270	59.549	40.451	0	0	0	0	0	0	0	0	0	0	0	0
FEBRA20074580	17.81	24.196	0	0	0	0	0	0	0	0	0	0	0	0
HRDPC20000550	15.129	10.276	0	0	0	0	0	0	14.505	9.705	0	0	0	0

[illegible]

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Table 36

FEBR20076220	7.094	1.606	4.614	1.519	0	1.465	0	0	0	0	1.517	2.382	0	0
HSTR20002480	4.385	9.928	2.852	1.878	0	0	0	0	0	0	1.875	0	0	0
TMK3220014350	4.337	2.946	4.232	5.572	0	0	4.612	0	0	0	0	0	0	0
ME SAN20001460	4.116	5.596	8.037	0	0	0	0	0	0	15.797	0	8.298	0	22.218
NUMPC20002060	0.878	1.192	1.713	0	0	0	0	0	0	1.09	1.683	0	0	0
NT2NE10000180	4.752	6.455	9.211	0	0	17.682	0	5.901	0	0	12.193	0	0	0
NT2NE20003920	24.178	24.087	9.435	4.142	0	1.997	0	2.002	0	8.272	3.247	9.413	0	0
NT2RR20006650	14.42	6.53	18.758	0	0	10.223	0	0	0	0	0	0	0	0
NT2R120013850	1.701	1.485	2.147	1.413	2.152	0	2.34	0	0	0	2.216	0	0	0
NT2R120014500	8.705	14.501	5.207	3.428	0	16.531	11.351	6.628	5.117	20.542	0	0	0	0
NT2R120025540	5.906	8.024	28.812	0	0	3.659	0	0	0	0	5.95	0	0	0
NT2R120033010	13.235	17.981	51.651	0	0	0	0	0	0	0	0	0	0	0
NT2R120075720	9.059	3.077	22.096	0	0	0	4.817	2.812	0	0	0	4.409	0	0
NT2RR60000350	1.407	2.868	9.611	0	0	0.872	0	0	0	2.708	0	0	0	0
NT2RR6001720	25.971	10.982	5.233	0	0	3.342	5.736	0	0	3.46	0	0	0	0
NT2RR70028760	4.927	7.780	14.402	3.161	3.206	1.016	8.721	0	0	5.261	4.957	3.193	4.424	0
NT2RR70029640	3.211	2.181	6.265	2.053	0	9.947	0	1.994	0	4.12	6.47	3.126	0	0
NT2RR70030300	18.559	6.297	18.098	0	0	0	14.787	5.756	0	0	0	4.511	0	0
NTONG00003340	6.944	9.434	13.519	8.922	13.581	0	0	0	0	0	0	0	0	0
OC68F00001100	3.85	15.681	22.537	0	0	0	0	0	0	0	0	0	0	0
OC68F00027310	8.987	6.1	25.295	0	0	5.564	9.55	11.153	0	11.522	0	0	0	0
OC68F20003040	29.316	13.276	19.088	0	0	0	0	0	0	0	0	0	0	0
SVAMP20000650	7.095	7.229	10.392	0	0	0	0	0	0	2.278	3.573	0	9.567	0
SVAMP20003960	3.493	1.413	9.382	0	0	0	0	0	0	0	0	0	0	0
LES1720023320	6.566	8.92	12.611	0	0	0	0	0	0	0	0	13.228	0	0
LES1720080200	4.328	1.959	7.033	0.926	0	0	9.2	0.895	0	1.85	0	0	3.889	0

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Table 37

	Clone ID	FEHRT	HEART
5	KIDNE20062480	36.242	0
	NT2R120033040	40.301	0
	NT2RP60000350	32.381	0
10	BGGI120010970	0	9.222
	BRACE10000420	0	23.223
	BRACE10001150	0	1.324
	BRACE20003320	0	31.422
15	BRACE20077980	0	15.184
	BRAWH10000370	0	65.363
	BRAWH20000340	0	22.282
	BRAWH20011660	0	6.271
20	BRAWH20014840	0	16.703
	FEBRA20008740	0	7.73
	FEBRA20072800	0	74.711
	HEART20000350	0	100
25	HEART20000990	0	100
	HEART20003090	0	100
	HEART20004110	0	100
	HEART20004480	0	100
30	HEART20004920	0	100
	HEART20005080	0	58.813
	HEART20005200	0	100
	HEART20005680	0	100
35	HHDP20001150	0	23.261
	HLUNG20005010	0	5.241
	HSYRA20014200	0	12.434
	IMR3220013170	0	9.002
40	KIDNE20004970	0	26.564
	NT2RI20000640	0	3.219
	NT2RI20006710	0	5.218
	NT2RI20015400	0	0.593
45	NT2RI20026540	0	8.062
	NT2RI20037510	0	5.211
	NT2RI20057230	0	20.346
	NT2RI20064120	0	17.978
50	NT2RI20071330	0	14.303
	NT2RI20071480	0	24.983
	NT2RI20077540	0	60.787
	NT2RI20084810	0	13.301
55	NT2RI20087910	0	6.007
	NT2RP70000760	0	9.681
	NT2RP70024500	0	41.168
	NT2RP70029060	0	6.444
	NTONG10001820	0	13.117
	PLACE60012810	0	32.247
	PLACE60043120	0	8.491
	PROST20000530	0	23.813
	SKMUS10000640	0	27.233
	SKMUS20004580	0	8.731

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Table 37 (continued)

Clone ID	FEHRT	HEART
SKMUS20015010	0	18.378
SMINT20002770	0	6.315
TEST120033250	0	58.713
TEST120074640	0	25.552
UMVEN20001330	0	6.282

Table 38

Clone ID	FEKID	KIDNE
3NB6920003300	0	2.071
3NB69200009120	0	2.884
BGG1120010970	0	4.336
BRACE20004210	0	3.583
BRACE20005250	0	6.242
BRACE20011170	0	3.303
BRACE20020910	0	19.111
BRACE20026850	0	34.356
BRACE20080970	0	20.33
BRAWH20000340	0	10.476
BRAWH20006970	0	3.96
BRAWH20011660	0	5.897
FCBBF20001950	0	65.363
FEBRA20021940	0	1.687
FEBRA20043250	0	12.177
HLUNG10000640	0	23.921
IMR3220007420	0	2.375
IMR3220014350	0	4.092
KIDNE10000280	0	100
KIDNE10000500	0	15.868
KIDNE10001040	0	100
KIDNE10001430	0	100
KIDNE10001450	0	19.052
KIDNE10001520	0	100
KIDNE20000410	0	100
KIDNE20000510	0	100
KIDNE20000700	0	100
KIDNE20000850	0	4.788
KIDNE20001670	0	100
KIDNE20001920	0	100
KIDNE20002440	0	37.565
KIDNE20002450	0	100
KIDNE20002660	0	7
KIDNE20003150	0	100
KIDNE20003300	0	20.536
KIDNE20003490	0	64.026
KIDNE20003750	0	100
KIDNE20004030	0	5.561
KIDNE20004220	0	35.77
KIDNE20004970	0	12.49

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Table 38 (continued)

Clone ID	FEKID	KIDNE
5	KIDNE20005130	0 100
	KIDNE20005170	0 81.524
	KIDNE20005190	0 100
	KIDNE20005740	0 2.3
	KIDNE20031850	0 16.193
10	KIDNE20033050	0 3.381
	KIDNE20033350	0 100
	KIDNE20033570	0 53.825
	KIDNE20033730	0 100
	KIDNE20033770	0 100
15	KIDNE20037520	0 100
	KIDNE20039410	0 100
	KIDNE20039940	0 43.968
	KIDNE20040340	0 100
	KIDNE20040540	0 49.114
20	KIDNE20040840	0 100
	KIDNE20042620	0 100
	KIDNE20042940	0 100
	KIDNE20042950	0 100
	KIDNE20043440	0 100
25	KIDNE20045200	0 100
	KIDNE20045340	0 17.53
	KIDNE20045790	0 100
	KIDNE20046810	0 100
	KIDNE20048280	0 100
30	KIDNE20048640	0 34.264
	KIDNE20048790	0 100
	KIDNE20049810	0 100
	KIDNE20050420	0 35.626
	KIDNE20052960	0 100
35	KIDNE20053360	0 58.142
	KIDNE20054000	0 49.697
	KIDNE20054770	0 100
	KIDNE20056290	0 100
	KIDNE20056760	0 16.262
40	KIDNE20059080	0 100
	KIDNE20059370	0 88.03
	KIDNE20060140	0 13.852
	KIDNE20060300	0 2.906
	KIDNE20060530	0 100
45	KIDNE20060620	0 100
	KIDNE20061490	0 100
	KIDNE20062480	0 2.972
	KIDNE20062990	0 31.685
	KIDNE20063530	0 26.747
50	KIDNE20063760	0 100
	KIDNE20066520	0 70.185
	KIDNE20067600	0 100
	KIDNE20067750	0 8.487
	KIDNE20068800	0 24.137

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Table 38 (continued)

	Clone ID	FEKID	KIDNE
5	KIDNE20070050	0	66.711
	KIDNE20070770	0	100
	KIDNE20071860	0	39.822
	KIDNE20073280	0	4.537
	KIDNE20073520	0	8.83
10	KIDNE20073560	0	100
	KIDNE20074220	0	100
	KIDNE20075690	0	100
	KIDNE20078100	0	100
	KIDNE20078110	0	100
15	LIVER10000790	0	15.673
	MAMGL10000320	0	1.138
	NB9N410000470	0	3.598
	NT2NE20053710	0	1.127
	NT2RI20006710	0	2.454
20	NT2RI20013420	0	2.015
	NT2RI20016570	0	23.435
	NT2RI20018460	0	20.967
	NT2RI20025540	0	5.573
	NT2RI20040590	0	13.676
25	NT2RI20065530	0	3.41
	NT2RI20087490	0	1.408
	NT2RI20087910	0	2.824
	NT2RP60000350	0	5.311
	NT2RP60001230	0	5.09
30	NT2RP70043730	0	14.846
	NT2RP70069860	0	10.745
	NT2RP70074220	0	3.96
	OCBBF20014940	0	49.164
	PLACE60014430	0	4.704
35	PLACE60020840	0	2.658
	PLACE60043120	0	3.992
	PROST10003430	0	25.547
	SKNMC20000970	0	1.143
	SKNSH20001510	0	20.208
40	SMINT10000160	0	38.817
	SMINT20003960	0	1.625
	SPLEN20000470	0	66.711
	SPLEN20001340	0	88.909
	SPLEN20003570	0	31.635
45	STOMA10000470	0	17.849
	SYNOV10001280	0	6.616
	TEST110000700	0	25.214
	TESTI20027070	0	14.795
	TESTI20040310	0	2.58
50	TRACH10000300	0	11.119
	TRACH20000790	0	4.534
	TRACH20002500	0	35.282
	TRACH20007800	0	5.605
	KIDNE10000080	77.87	22.13

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Table 38 (continued)

Clone ID	FEKID	KIDNE
KIDNE20044110	92.49	7.51
NT2R120033040	40.707	0
NT2R120037510	60.346	0
NT2RP70065270	40.543	0
TRACH20012890	52.552	0

Table 39

Clone ID	FELNG	HLUNG
BNGH410001980	0	16.113
BRACE10000420	0	7.831
BRACE10001150	0	1.339
BRACE20014770	0	28.126
BRACE20018550	0	25.65
BRAWH20006970	0	8.521
BRAWH20014610	0	7.03
FEBRA20008810	0	19.713
FEBRA20015840	0	53.019
FEBRA20044120	0	15.75
HHDP20001490	0	25.611
HLUNG10000240	0	100
HLUNG10000300	0	100
HLUNG10000370	0	100
HLUNG10000640	0	51.466
HLUNG10000760	0	12.838
HLUNG10000990	0	100
HLUNG10001050	0	100
HLUNG10001100	0	100
HLUNG20000680	0	72.532
HLUNG20001160	0	100
HLUNG20001250	0	100
HLUNG20001420	0	79.349
HLUNG20001760	0	100
HLUNG20002550	0	100
HLUNG20003140	0	14.018
HLUNG20004120	0	42.131
HLUNG20004800	0	100
HLUNG20005010	0	5.302
HSYRA20014200	0	12.578
KIDNE20002660	0	15.061
KIDNE20033050	0	3.637
NT2NE20014350	0	28.99
NT2R120016570	0	9.167
NT2R120026540	0	8.156
NT2R120051500	0	21.652
NT2R120064120	0	9.093
NT2R120083960	0	17.851
NT2R120085260	0	5.474
NT2R120087490	0	3.03

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Table 39 (continued)

Clone ID	FELNG	HLUNG
NT2RP70009060	0	18.337
NT2RP70011660	0	5.822
NT2RP70029060	0	6.519
NT2RP70055020	0	10.451
NT2RP70074220	0	8.521
NT2RP70076100	0	25.546
NTONG10002460	0	16.426
NTONG20008000	0	7.189
PLACE60043120	0	8.589
SKMUS20016340	0	15.317
SKNMC20005930	0	13.727
SMINT20000180	0	38.989
SMINT20002390	0	51.283
SMINT20002770	0	12.776
SMINT20003960	0	10.489
STOMA10000470	0	38.402
STOMA20001880	0	52.43
SYNOV20013740	0	23.798
TESTI20036250	0	32.684
TESTI20080200	0	2.927
TRACH20004610	0	28.395
BRACE20004210	86.645	0
IMR3220007420	57.437	0

Table 40

Alteration of the expression level of each clone due to TNF- α or LPS stimulation to human monocyte cell line THP-1 and alteration of the expression level of each clone due to co-culture of gastric cancer cell line MKN45 with *Helicobacter pylori*. ctl, TNF and LPS in the column of THP-1, respectively, indicate the relative expression levels in unstimulated THP-1, in the cell stimulated with 10 ng/mL TNF- α for 3 hours, and in the cell stimulated with 1 μ g/mL LPS for 3 hours; ctl and *H. pylori* in the column of MKN45 indicate the relative expression levels in MKN45 cultured without *Helicobacter pylori* and in MKN45 co-cultured with *Helicobacter pylori* (at a ratio of MKN45: *Helicobacter pylori* = 1:100 cells (colonies) for 3 hours, respectively [ATAC-PCR]

Clone name	THP-1			MKN45	
	ctl	TNF	LPS	ctl	<i>H. pylori</i>
3NB6920000290	2.0	1.9	0.4	0.1	0.0
ADRG10000180	2.2	5.1	2.0	3.3	5.7
BNGH410001370	0.8	1.4	0.3	0.4	0.5
BRACE10001590	1.5	2.3	1.6	0.4	0.8
BRACE10001690	2.3	3.6	2.9	2.2	1.8
BRACE20010650	2.1	2.2	2.1	2.2	2.1
BRACE20013400	2.6	0.8	0.2	1.5	1.1
BRACE20030780	0.3	1.3	0.0	2.2	1.7
BRACE20034490	2.0	1.6	0.6	2.5	0.3
BRACE20077640	0.4	1.0	0.1	1.7	0.3
BRACE20079530	0.6	0.1	0.1	0.0	0.2
BRACE20083850	0.9	2.5	1.3	1.1	0.0
BRACE20091880	1.5	0.5	0.1	0.5	0.0

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Table 40 (continued)

	Clone name	THP-1			MKN45	
		ctl	TNF	LPS	ctl	H.pylori
5	BRAWH10001620	1.8	1.0	0.3	1.1	3.1
	BRAWH20004430	0.2	1.4	0.2	0.5	0.5
	FCBBF10006180	0.1	3.6	1.3	2.1	0.7
	FEBRA20003780	1.5	3.0	2.8	1.7	1.3
10	FEBRA20006800	0.7	2.4	0.9	0.0	1.6
	FEBRA20008810	2.3	1.4	0.9	2.3	1.3
	FEBRA20012940	0.4	1.0	0.2	0.7	0.6
	FEBRA20015840	0.1	3.3	2.6	0.1	0.0
15	HCASM10000610	1.8	2.0	2.1	2.3	2.2
	HEART20000350	2.0	3.3	1.8	2.3	0.5
	HEART20004480	0.0	0.3	0.0	3.5	3.0
	HEART20005060	1.2	0.6	0.0	4.8	4.5
20	HHDP20000950	0.4	0.2	0.1	1.4	0.7
	HLUNG10000370	0.0	1.3	0.2	2.6	0.7
	HLUNG20001160	0.6	3.7	1.7	0.1	0.0
	HLUNG20001760	1.4	0.5	0.0	0.3	0.0
25	HSYRA20003470	1.1	1.5	0.6	1.1	0.3
	HSYRA20013320	0.1	1.7	0.7	1.4	0.7
	IMR3210001580	0.4	0.0	0.0	0.3	0.2
	IMR3210002660	0.8	0.4	0.2	0.5	0.4
30	IMR3220008380	0.4	0.9	0.4	1.1	0.5
	IMR3220008590	2.0	0.3	0.9	2.1	3.4
	KIDNE10001520	0.4	1.2	0.7	3.4	2.2
	KIDNE20000850	0.7	0.7	0.4	1.1	0.5
35	KIDNE20003490	0.9	1.7	0.9	0.3	1.9
	KIDNE20005170	0.9	0.7	0.3	6.4	0.2
	KIDNE20033730	1.2	1.6	1.8	0.5	0.5
	KIDNE20040540	0.1	2.5	0.8	0.1	0.2
40	KIDNE20050420	0.7	0.5	0.7	0.2	0.3
	KIDNE20061490	0.1	1.2	0.6	0.2	0.1
	KIDNE20062990	0.7	3.5	0.7	0.0	0.0
	LIVER20000330	6.0	7.4	1.1	7.3	0.6
45	NT2NE10001630	0.1	2.6	1.4	2.5	2.7
	NT2NE10001850	1.1	0.3	0.1	0.4	1.1
	NT2NE20003920	0.6	3.3	1.6	0.5	0.2
	NT2NE20005500	0.6	2.6	2.2	0.1	0.2
50	NT2RI20009740	1.2	1.9	0.9	0.1	0.0
	NT2RI20014500	0.2	3.5	1.7	0.0	0.0
	NT2RI20016570	1.2	3.6	3.1	0.0	0.1
	NT2RI20018660	4.3	0.5	1.3	1.9	1.8
55	NT2RI20021520	1.1	1.5	1.1	1.1	0.5
	NT2RI20050870	1.0	0.6	0.3	0.7	0.8
	NT2RI20053350	2.2	1.0	0.9	1.5	0.6
	NT2RI20070480	1.5	0.3	0.0	0.0	0.0
	NT2RI20073030	0.4	0.6	0.4	2.0	0.8
	NT2RI20078270	0.2	2.6	0.5	1.4	0.3
	NT2RI20078790	1.7	2.4	0.7	2.2	1.6
	NT2RI20083360	0.1	0.4	0.2	0.1	0.3

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Table 40 (continued)

	Clone name	THP-1			MKN45	
		ctl	TNF	LPS	ctl	H.pylori
5	NT2RP60000080	2.2	2.5	1.5	2.0	1.1
	NT2RP60000390	1.6	2.3	1.2	2.3	0.4
	NT2RP60000590	1.6	2.0	1.3	2.5	1.3
	NTONG10000980	0.9	0.8	0.8	1.9	0.0
10	NTONG10002570	0.1	5.4	0.5	0.0	0.0
	PLACE60020160	0.8	1.2	0.6	0.0	0.0
	PLACE60026990	0.5	0.2	0.1	3.2	2.1
	PLACE60047380	1.6	0.7	0.9	1.8	2.2
15	PUAEN10003220	0.1	1.9	1.2	0.0	0.1
	SKNMC10000290	0.4	1.2	0.5	0.9	0.2
	SKNMC10001590	1.7	1.9	0.8	1.0	0.4
	SKNMC20000650	1.1	1.1	0.8	0.1	0.1
20	STOMA20002570	0.3	3.1	1.5	0.6	0.6
	STOMA20002890	1.8	0.8	0.4	0.1	0.2
	SYNOV20001770	1.7	0.5	0.5	1.7	4.2
	TEST11000230	2.7	4.6	3.1	2.3	1.7
25	TEST110000550	0.4	0.1	0.3	0.1	2.8
	TEST120011340	0.3	2.3	2.2	2.2	1.9
	THYMU10005580	1.1	2.1	1.1	1.5	1.1
	TRACH10000630	0.3	0.5	0.2	2.7	2.6
30	TRACH20001960	9.4	2.7	1.3	1.0	0.4
	UMVEN10001220	1.9	2.8	1.0	0.8	0.2
	UMVEN20001330	2.2	2.2	0.0	1.0	0.1
	UTERU20004850	1.7	6.3	2.3	0.0	0.3

Homology Search Result Data

- 35 [0295] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequences.
- [0296] In the result of the search shown below, both units, aa and bp, are used as length units for the sequences to be compared.
- 40 [0297] Each data includes Clone name, Definition in hit data, P value, Length of sequence to be compared, Homology, and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash mark, //.
- 3NB6910000180
3NB6910000850
3NB6910001160//STEROIDOGENIC ACUTE REGULATORY PROTEIN PRECURSOR./19.70E-08//160aa//21%//Q28996
- 45 3NB6910001290
3NB6910001730
3NB6920000290
3NB6920002810//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III./4.70E-154//442aa//64%//P34580
- 50 3NB6920003300//YIP1 PROTEIN./1.80E-35//181aa//41%//P53039
3NB6920005450
3NB6920009120
3NB6920010020//REGULATOR OF G-PROTEIN SIGNALING 3 (RGS3) (RGP3)/1.60E-89//179aa//95%//P49796
3NB6920010220//putative C3HC4-type RING zinc finger protein/3.70E-38//374aa//29%//AAG27460
- 55 3NB6920013490
3NB6920014330
3NB6920014710//Homo sapiens hepatocellular carcinoma-associated antigen 58 (HCA58) mRNA, complete cds./5.40E-130//236aa//100%//AF220416

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- 3NB6920015110//CARG-BINDING FACTOR-A (CBF-A) //7.50E-140//290aa//90%//Q99020
- 3NB6920015280//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1 //4.60E-55//263aa//35%//P48732
- 3NB6920015570//ZINC FINGER PROTEIN 135 //7.90E-129//365aa//60%//P52742
- 3NB6920016370
- 3NB6920017190
- 5 ADRGL10000020//Homo sapiens Kelch-like 1 protein (KLHL1) mRNA, complete cds.//2.90E-298//546aa//100%//AF252283
- ADRGL10000180
- ADRGL10000650//ZING FINGER PROTEIN 135 //2.20E-76//205aa//64%//P52742
- 10 ADRGL10001600//CYTOCHROME P450 XXIB (EC 1.14.99.10) (STEROID 21-HYDROXYLASE) (P450-C21B) //2.50E-248//397aa//98%//P08666
- ADRGL10001650//IMIDAZOLONEPROPIONASE (EC 3.5.2.7) (IMIDAZOLONE-5-PROPIONATE HYDROLASE) //6.10E-67//418aa//37%//P42084
- ADRGL10001820
- 15 A0R6L20000740//RHO-GTPASE-ACTIVATING PROTEIN 6 (RHO-TYPE GTPASE-ACTIVATING PROTEIN RHOG-APX-1) //1.50E-67//327aa//43%//O43182
- ADRGL20003230
- ADRGL20004280
- ASTR010000180//DYNEIN INTERMEDIATE CHAIN 3, CILIARY //1.10E-32//207aa//33%//O16960
- 20 ASTR020000950
- ASTR020004170//Homo sapiens sorting nexin 5 (SNX5) mRNA, complete cds.//5.20E-47//98aa//100%//AF121855
- ASTR020004800
- BGGI110002850
- BGGI120001610//CELL DIVISION CONTROL PROTEIN 1 //3.10E-14//218aa//28%//P40986
- 25 BGGI120005330//INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE 2 (EC 1.1.1.205) (IMP DEHYDROGENASE 2) (IMPDH-II) (IMPD 2) //1.40E-218//415aa//80%//P12269
- BGGI120005440//Homo sapiens snurportin1 mRNA, complete cds.//3.50E-199//360aa//99%//AF039029
- BGGI120006840//Homo sapiens sirutin 2 (SIRT2) mRNA, complete cds.//7.60E-197//371aa//98%//AF083107
- BGGI120006930//POLYHOMEOTIC-PROXIMAL CHROMATIN PROTEIN //2.30E-11//100aa//42%//P39769
- 30 BGGI120010970//Homo sapiens contactin associated protein (Casp) mRNA, complete cds.//3.50E-103//464aa//36%//U87223
- BGGI120017140//ZINC FINGER PROTEIN 124 (HZF-16) //1.60E-127//217aa//100%//Q15973
- BNGH410000030//R. norvegicus trg mRNA.//3.10E-111//361aa//60%//X68101
- BNGH410000130
- 35 BNGH410000170
- BNGH410000290
- BNGH410000330
- BNGH410000340//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (THYMOCYTE-ACTIVATING MOLECULE) (THAM) //3.20E-36//262aa//38%//P28843
- 40 BNGH410000390//DYNEIN BETA CHAIN, CILIARY //4.60E-136//331aa//72%//P23098
- BNGH410000800//Homo sapiens zinc finger protein dp mRNA, complete cds.//2.80E-11//103aa//41%//AF153201
- BNGH410001040
- BNGH410001180//Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDI) mRNA, complete cds.//0.752aa//96%//AF176832
- 45 BNGH410001370//BRUSH BORDER 61.9 KD PROTEIN PRECURSOR //6.30E-72//555aa//31%//Q05004
- BNGH410001530
- BNGH410001770//INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE 1 (EC 1.1.1.205) (IMP DEHYDROGENASE 1) (IMPDH-I) (IMPD 1) //2.10E-270//514aa//99%//P20839 BNGH410001900//Rattus norvegicus schlafen-4 (SLFN-4) mRNA, complete cds.//3.80E-81//568aa//35%//AF168795
- 50 BNGH410001980//TETRACYCLINE RESISTANCE PROTEIN, CLASS E (TETA(E)) //1.20E-15//345aa//26%//Q07282
- BNGH4200004740
- BNGH420005320//ZINC FINGER PROTEIN 36 (ZINC FINGER PROTEIN KOX18) (FRAGMENT) //6.40E-179//322aa//99%//P17029
- BRACE10000200
- 55 BRACE10000420//PROTEIN PHOSPHATASE 2C ABI2 (EC 3.1.3.16) (PP2C) //2.10E-31//202aa//37%//O04719
- BRACE10000700
- BRACE10000730//HYPOTHETICAL 37.2 KDA PROTEIN C12C2.09C IN CHROMOSOME II //9.60E-05//100aa//34%//Q09749

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BRACE10000930//TNF RECEPTOR ASSOCIATED FACTOR 2 (TRAF2) //2.10E-96//197aa//92%//P39429
 BRACE10001150//NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 2 (BRAIN-SPECIFIC PROTEIN, X- LINKED) //3.60E-17//144aa//36%//P51860
 5 BRACE10001590
 BRACE10001660
 BRACE10001690
 BRACE10001870//MICROTUBULE-ASSOCIATED PROTEIN 4 //8.30E-12//49aa//81%//P27816
 BRACE20000770
 BRACE20001000
 10 BRACE20001410
 BRACE20002800//MNN4 PROTEIN //8.50E-10//237aa//29%//P36044
 BRACE20003320
 BRACE20004210
 BRACE20005050
 15 BRACE20005250//DDR1 PROTEIN (TU3A PROTEIN) //5.20E-74//144aa//100%//095990
 BRACE20005450
 BRACE20005650
 BRACE20005770//Homo sapiens PHR1 isoform 4 (PHRET1) mRNA, alternatively spliced, complete cds.//5.80E-48//91aa//100%//AF093249
 20 BRACE20006980//ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN, NONERYTHROID) //2.40E-16//279aa//30%//Q01484
 BRACE20007180//CALCITONIN GENE-RELATED PEPTIDE II PRECURSOR (CGRP-II) (BETA-TYPE CGRP) //2.70E-61//127aa//99%//P10092
 BRACE20008850//CALDESMON (CDM) //3.50E-08//203aa//29%//P12957
 25 BRACE20009880
 BRACE20010650
 BRACE20010700
 BRACE20011170
 BRACE20011430//Zea mays clone AGP2m1 arabinogalactan protein (agp) mRNA, partial cds.//3.70E-06//176aa//33%//AF134579
 30 BRACE20011880
 BRACE20013400
 BRACE20013520
 BRACE20013740
 35 BRACE20013750
 BRACE20014230
 BRACE20014530//38.4 KDA PROLINE-RICH PROTEIN //5.50E-10//102aa//34%//Q00451
 BRACE20014550//HEAT SHOCK FACTOR PROTEIN 1 (HSF 1) (HEAT SHOCK TRANSCRIPTION FACTOR 1) (HSTF 1) //1.00E-118//229aa//99%//Q00613
 40 BRACE20014770//HUNTINGTIN ASSOCIATED PROTEIN 1 (HAP1) //1.70E-22//81aa//39%//P54256
 BRACE20014920//PROTEIN-TYROSINE PHOSPHATASE-LIKE N PRECURSOR (R-PTP-N) (ISLET CELL AUTOANTIGEN 512) (ICA512) //3.10E-42//110aa//84%//P56722
 BRACE20015080//PROTEIN-LYSINE 6-OXIDASE PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE) //1.30E-06//110aa//35%//Q05063
 45 BRACE20015430
 BRACE20016730//Mus musculus mdgl-1 mRNA, complete cds.//3.00E-54//118aa//83%//AF190624
 BRACE20016920
 BRACE20017370//P.vivax pva1 gene.//2.70E-20//99aa//49%//X92485
 BRACE20018550//B-CELL LYMPHOMA 3-ENCODED PROTEIN (BCL-3 PROTEIN) //9.20E-16//300aa//30%//P20749
 50 BRACE20018590//NOVEL ANTIGEN 2 (NAG-2) (TSPAN-4) //8.30E-28//69aa//91%//Q014817
 BRACE20018650
 BRACE20018980
 BRACE20019440
 55 BRACE20020500
 BRACE20020910//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN) //1.10E-31//91aa//49%//Q62158
 BRACE20021510
 BRACE20021760

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BRACE20022020/SERINE/THREONINE-PROTEIN KINASE SNK (EC 2.7.1.-) (SERUM INDUCIBLE KINASE).//
1.60E-41//102aa//47%//P53351
BRACE20022270
BRACE20024090/HOMEOBOX PROTEIN MEIS3 (MEIS1-RELATED PROTEIN 2).//1.50E-108//210aa//89%//
5 P97368
BRACE20024310/P53-INDUCED PROTEIN 11.//5.00E-37//111aa//69%//014683
BRACE20024680/Homo sapiens GalNAc-T9 mRNA for UDP-GalNAc:polypeptide N-acetylglucosaminyltrans-
ferase, complete cds.//3.00E-153//244aa//99%//AB040672
BRACE20024780/NEURALIZED PROTEIN.//1.20E-14//95aa//38%//P29503
10 BRACE20024960
BRACE20025900
BRACE20026350/SODIUM/NUCLEOSIDE COTRANSPORTER (NA(+)/NUCLEOSIDE COTRANSPORTER).//
3.40E-25//53aa//96%//P26430
BRACE20026850/Homo sapiens androgen-regulated short-chain dehydrogenase/reductase 1 (ARSDR1) mRNA,
15 complete cds.//6.50E-120//313aa//72%//AF167438
BRACE20027360/Homo sapiens mRNA for fructosamine-3-kinase (FN3K gene).//3.00E-80//150aa//91%//AJ404615
BRACE20027520
BRACE20027550/REGULATOR OF MITOTIC SPINDLE ASSEMBLY 1 (RMSA-1).//1.40E-19//128aa//44%//P49646
BRACE20027720/HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6) (GLYOXALASE II) (GLX II).//2.50E-
20 35//133aa//50%//Q16775
BRACE20027920/L-RIBULOKINASE (EC 2.7.1.16).//5.20E-40//387aa//29%//P94524
BRACE20027960/Rattus norvegicus neurabin mRNA, complete cds.//2.70E-10//48aa//86%//U72994
BRACE20028120/Mus musculus GTPase Rab37 (Rab37) mRNA, complete cds.//4.60E-48//129aa//78%//AF233582
BRACE20028600
25 BRACE20028610
BRACE20028960/Mus musculus mRNA for Ca2+ dependent activator protein for secretion, complete cds.//6.10E-
195//473aa//74%//D86214
BRACE20030780
BRACE20031100/PATCHED PROTEIN HOMOLOG 1 (PTC1) (PTC).//3.00E-23//234aa//25%//Q61115
30 BRACE20032850
BRACE20033190
BRACE20033980
BRACE20034310
BRACE20034490
35 BRACE20035160
BRACE20035270
BRACE20035390
BRACE20035940
BRACE20071380/PR0B CALCIUM-TRANSPORTING ATPASE 3 (EC 3.6.1.38) (ENDOPLASMIC RETICULUM
40 CA2+-ATPASE).//3.50E-65//343aa//39%//P39524
BRACE20071530
BRACE20071740/ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//4.90E-157//380aa//61%//P51523
BRACE20071970
BRACE20072010
45 BRACE20072320
BRACE20072810
BRACE20074010/Oryctolagus cuniculus peroxisomal Ca-dependent solute carrier mRNA, complete cds.//2.30E-
140//383aa//65%//AF004161
BRACE20074470/Mus musculus partial mRNA for mouse fat 1 cadherin (mfat1 gene). //3.90E-131//454aa//57%//
50 AJ250768
BRACE20075020
BRACE20075270
BRACE20075380
BRACE20075630
55 BRACE20076210
BRACE20076410/Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds.//5.10E-173//
320aa//94%//D64009
BRACE20076460

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- BRACE20078630//Dog nonerythroid beta-spectrin mRNA//1.60E-05//86aa//37%//L02897
 BRACE20078650//Homo sapiens cell cycle checkpoint protein CHFR mRNA, complete cds.//1.20E-54//104aa//99%//
 AF170724
- 5 BRACE20077080
 BRACE20077270
 BRACE20077610
 BRACE20077640
 BRACE20077670
 BRACE20077680
- 10 BRACE20077840//Putative Protein that mediates attachment of autophagosomes to microtubules, by similarity to yeast
 aut12 [Schizosaccharomyces pombe]//1.00E-08//200aa//26%//CAC00556
 BRACE20077980
 BRACE20078680 PROTEIN.//2.40E-05//140aa//30%//P44678
 BRACE20078820//actin-depolymerizing protein N-WASP//5.50E-06//116aa//37%//S72273
- 15 BRACE20079020
 BRACE20079530
 BRACE20080970
 BRACE20081140
 BRACE20083800
- 20 BRACE20083850//Rattus norvegicus NRBF-2 mRNA for nuclear receptor binding factor-2, complete cds.//1.30E-135//
 288aa//90%//AB024930
 BRACE20084430//PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (EC 5.3.4.1) (PDIR).//
 8.30E-102//186aa//98%//Q14554
 BRACE20084800
- 25 BRACE20084880
 BRACE20086530
 BRACE20086550//Homo sapiens mRNA for GABAB receptor, subunit 1b.//8.30E-22//55aa//90%//AJ012186
 BRACE20087080
 BRACE20087540
- 30 BRACE20088570
 BRACE20089600
 BRACE20089990
 BRACE20090140
 BRACE20091880//Mus musculus mRNA for synaptotagmin V, complete cds.//9.90E-85//166aa//96%//AB026802
- 35 BRACE20092120
 BRACE20092740
 BRACE20092750
 BRACE20093070//P120 PROTEIN.//1.40E-13//121aa//41%//P30999
 BRACE20093110
- 40 BRACE20093610
 BRACE20094370
 BRACE20095170
 BRAWH10000010//Homo sapiens PMEPA1 protein (PMEPA1) mRNA, complete cds.//2.00E-84//250aa//67%//
 AF224278
- 45 BRAWH10000020//Homo sapiens putative hepatic transcription factor (WBSCR14) mRNA, complete cds.//1.20E-168//
 345aa//89%//AF156803
 BRAWH10000070
 BRAWH10000370//UROKINASE PLASMINOGEN ACTIVATOR SURFACE RECEPTOR PRECURSOR (U-PAR)
 (CD87).//9.40E-08//155aa//29%//005588
- 50 BRAWH10000940//Xenopus laevis mRNA for Nfr1, complete cds.//6.10E-257//606aa//77%//D86491
 BRAWH10001300
 BRAWH10001620//Rattus norvegicus development-related protein mRNA, complete cds.//1.90E-115//339aa//93%//
 AF045564
 BRAWH10001640//Homo sapiens KRAB zinc finger protein (RITA) mRNA, complete cds.//5.10E-14//57aa//88%//
 AF272148
- 55 BRAWH10001680//Homeotic protein emx2//9.60E-126//252aa//92%//151737
 BRAWH10001740
 BRAWH10001800

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- BRAWH20000340//TRP-185 protein//7.20E-28//68aa//97%//S62356
- BRAWH20000480//Mus musculus kinesin motor protein KIFC2 mRNA, complete cds.//1.50E-120//270aa//85%//U92949
- 5 BRAWH20000930
- BRAWH20001090//SARCALUMENIN PRECURSOR.//1.90E-05//363aa//24%//P13666
- BRAWH20001770//SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (EC 2.1.2.1) (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) //3.20E-41//77aa//100%//P34897
- BRAWH20002480
- BRAWH20003230//Proline rich protein//2.00E-29//142aa//52%//CAA48321
- 10 BRAWH20004430//Human breast cancer, estrogen regulated LIV-1 protein (LIV-1) mRNA, partial cds.//1.00E-46//164aa//46%//U41060
- BRAWH20004760//Mus musculus mRNA for Eos protein, complete cds.//1.80E-92//160aa//92%//AB017615
- BRAWH20005030//REGULATOR OF MITOTIC SPINDLE ASSEMBLY 1 (RMSA-1) //6.50E-18//103aa//52%//P49646
- BRAWH20005220//Homo sapiens hD54+ins2 isoform (hD54) mRNA, complete cds.//1.20E-77//206aa//50%//AF004430
- 15 BRAWH20005540
- BRAWH20006330//Homo sapiens mRNA for zinc finger 2 (ZNF2 gene) //1.20E-120//214aa//98%//X60152
- BRAWH20006510//HYDROXYMETHYLGLUTARYL-COA LYASE (EC 4.1.3.4) (HMG-COA LYASE) (HL) (3-HYDROXY-3-METHYLGLUTARATE-COA LYASE) //1.60E-96//238aa//73%//P35915 BRAWH20006660//SERINE/THREONINE-PROTEIN KINASE SGK (EC 2.7.1.-) (SERUM/GLUCOCORTICOID-REGULATED KINASE) //4.20E-223//406aa//99%//000141
- 20 BRAWH20006970
- BRAWH20008660
- BRAWH20008920
- 25 BRAWH20009010//Human (c-myc) gene, complete primary cds, and five complete alternatively spliced cds.//9.70E-28//105aa//59%//U22376
- BRAWH20009440//Arabidopsis thaliana pollenless3 (17b) gene, complete cds; beta-9 tubulin (TUB9) gene, partial cds; and unknown gene //7.90E-31//271aa//34%//AF060248
- BRAWH20009840//CYTOCHROME P450 2J2 (EC 1.14.14.1) (CYP11J2) (ARACHIDONIC ACID EPOXYGENASE) //1.10E-146//273aa//98%//P51589
- 30 BRAWH20011030
- BRAWH20011290//OCCLUDIN //2.90E-07//174aa//29%//Q61146
- BRAWH20011410//CUTICLE COLLAGEN 2 //2.30E-05//129aa//35%//P17656
- BRAWH20011660//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE) //1.40E-105//421aa//49%//P16278
- 35 BRAWH20012030
- BRAWH20014180//Homo sapiens double-stranded RNA specific adenosine deaminase (ADAR3) mRNA, complete cds.//3.60E-97//179aa//100%//AF034837
- BRAWH20014380
- 40 BRAWH20014610
- BRAWH20014840//POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYLGLACTOSAMINYLTRANSFERASE) (UDP-GALNAc:POLYPEPTIDE, N-ACETYLGLACTOSAMINYLTRANSFERASE) (GALNAc-T1) //4.50E-84//511aa//36%//Q07537
- BRAWH20015030
- 45 BRAWH20036890//Mus musculus clone mouse1-9 putative protein phosphatase type 2C mRNA, partial cds.//2.70E-59//120aa//98%//AF117832
- BRAWH20036930
- BRAWH20038320
- BRAWH20040950
- 50 BRAWH20047310
- BRAWH20052250
- BRAWH20059980//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1) //8.60E-37//282aa//32%//P98070
- BRAWH20060440
- 55 BRAWH20064500//Homo sapiens CAGF9 mRNA, partial cds.//8.00E-25//148aa//51%//U80736
- BRAWH20064930
- BRAWH20066220//DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM.//3.20E-41//221aa//39%//Q39575
- BRAWH20069600

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- BRAWH20069890//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT)/J.9.50E-07//188aa//30%//P11414
BRAWH20074060
BRAWH20076050//LORICRIN/J.2.80E-05//160aa//31%//P18165
5 BRAWH20087060
BRAWH20089030
BRAWH20089560//Protein-tyrosine-phosphatase (EC 3.1.3.48)
TD14//0//736aa//90%//T14355
BRAWH20092270
10 BRAWH20092610//TLM PROTEIN (TLM ONCOGENE)/J.3.90E-15//122aa//43%//P17408
BRAWH20093600
BRAWH20094850
CD34C20000510//Human chitotriosidase precursor mRNA, complete cds/J.7.80E-247//366aa//98%//U29615
CTONG20003030
15 CTONG20005890//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSYN-110)/J.3.10E-18//241aa//31%//Q15700
CTONG20007710
CTONG20008270
CTONG20011390
20 CTONG20013200//HYPOTHETICAL PROTEIN C2G11.15C IN CHROMOSOME I (FRAGMENT)/J.1.60E-15//130aa//36%//Q09814
CTONG20013660//GLUGOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)/J.5.00E-11//468aa//23%//P08640
CTONG20015330
25 CTONG20018200//Mus musculus NSD1 protein mRNA, complete cds/J.0//1061aa//87%//AF064553
CTONG20019110//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLSTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG)/J.5.40E-19//116aa//39%//Q13107
30 CTONG20019550//Homo sapiens mRNA for actin binding protein ABP620, complete cds/J.0//1175aa//53%//AB029290
CTONG20020730
CTONG20021430
CTONG20024180//Homo sapiens scaffold attachment factor B (SAF-B) mRNA, partial cds/J.3.10E-52//366aa//40%//L43631
35 CTONG20024530
CTONG20025580//ZINC FINGER PROTEIN 211 (ZINC FINGER PROTEIN C2H2-25)/J.2.00E-58//223aa//45%//Q13398
CTONG20027210//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13/J.7.90E-06//224aa//24%//Q07878
40 CTONG20028030
CTONG20028160//Homo sapiens cadherin-like protein VR20 mRNA, partial cds/J.9.70E-170//290aa//100%//AF169690
CTONG20028200//Mus musculus MGA protein mRNA, complete cds/J.0//1132aa//85%//AF205935
CTONG20029650
45 CTONG20037820//GAMMA-AMINOBUTYRIC-ACID RECEPTOR PI SUBUNIT PRECURSOR (GABA(A) RECEPTOR)/J.4.30E-94//164aa//93%//U000591
CTONG20047160//Rattus norvegicus mRNA for seven transmembrane receptor, complete cds/J.1.10E-26//319aa//29%//AB019120
50 CTONG20055530//ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN, NONERYTHROID)/J.1.90E-59//598aa//30%//Q01484
CTONG20064490//Drosophila melanogaster 26S proteasome regulatory complex subunit p42A mRNA, complete cds/J.1.00E-41//108aa//77%//AF145308
D30ST20001840//RNA binding motif protein 9 [Homo sapiens]/J.1.00E-139//297aa//91%//INP_055124
DFNES20002120//Mus musculus tgi mRNA for tRNA-guanine transglycosylase, complete cds/J.1.40E-62//140aa//83%//AB034632
55 DFNES20002680//MYOSIN HEAVY CHAIN, STRIATED MUSCLE/J.9.00E-26//620aa//24%//P24733
DFNES20002920
DFNES20003350//CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER

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- PROTEIN 1) //5.30E-05//277aa//25%//Q06852
- DFNES20004320//Homo sapiens ubiquitous TPR-motif protein Y isoform (UTY) gene, partial cds; alternatively spliced //3.20E-15//85aa//50%//AF265575
- FCBBF10005980//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2) //3.20E-15//395aa//57%//P51523
- 5 FCBBF10006180
- FCBBF10006750
- FCBBF10006860
- FCBBF10006870//Mus musculus Rap2 interacting protein 8 (RPIP8) mRNA, complete cds //3.10E-113//456aa//53%//U73941
- 10 FCBBF10006910
- FCBBF10007320
- FCBBF10007600
- FCBBF20000940//MONOCYTIC LEUKEMIA ZINC FINGER PROTEIN (ZINC FINGER PROTEIN 220) //2.70E-05//194aa//28%//C92794
- 15 FCBBF20001050
- FCBBF20001950
- FCBBF20002320
- FCBBF20002760//ALPHA SCRUIIN //2.70E-05//214aa//24%//Q25390
- FCBBF20005760
- 20 FCBBF20005910//KINESIN LIGHT CHAIN (KLC) //6.40E-10//114aa//39%//P46825
- FCBBF20006770
- FCBBF20007330//DIPEPTIDYL PEPTIDASE IV LIKE PROTEIN (DIPEPTIDYL AMINOPEPTIDASE- RELATED PROTEIN) (DIPEPTIDYLPEPTIDASE VI) (DPPX-L/DPPX-S) //1.70E-19//86aa//45%//P46101
- 25 FCBBF20008080
- FCBBF20008150//ZYXIN //7.60E-57//350aa//34%//O04584
- FCBBF20009400
- FCBBF20009510//ZINC FINGER PROTEIN 7 (ZINC FINGER PROTEIN KOX4) (ZINC FINGER PROTEIN HF.16) //2.30E-76//225aa//43%//P17097
- 30 FCBBF20012110//Leishmania major partial ppgI gene for proteophosphoglycan //3.50E-05//256aa//24%//AJ243460
- FCBBF20012990
- FCBBF20014800
- FCBBF20015380//Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HEL01) mRNA, complete cds //7.00E-61//319aa//44%//AF231981
- 35 FCBBF20016720
- FCBBF20017180
- FCBBF20017200
- FCBBF40002820//ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT (BETA-ETF) //3.60E-121//239aa//99%//P38117
- 40 FCBBF50002610//ZINC FINGER PROTEIN 35 (ZFP-35) //1.40E-137//489aa//50%//P15620
- FEBRA20000350//Mus musculus MAST205 protein kinase mRNA, complete cds //6.20E-71//190aa//76%//U02313
- FEBRA20000530//Drosophila melanogaster Diabolo (dlo) mRNA, complete cds //6.40E-58//495aa//32%//AF237711
- FEBRA20001050//KINESIN LIGHT CHAIN (KLC) //4.20E-207//566aa//69%//O07866
- FEBRA20001290//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE (EC 2.1.1.61) //4.60E-43//82aa//100%//O75648
- 45 FEBRA20003110//Homo sapiens UDP-GlcNAc:alpha-3-D-mannoside b1,2-N-acetylglucosaminyltransferase 1.2 (MGAT1.2) mRNA, partial cds //3.80E-92//172aa//98%//AF250859
- FEBRA20003300
- FEBRA20003770//Homo sapiens ankyrin repeat-containing protein (CCM1) mRNA, complete cds //0//406aa//100%//AF296765
- 50 FEBRA20003780
- FEBRA20003910
- FEBRA20003970//ZINC FINGER PROTEIN 228 //1.60E-118//423aa//52%//Q9UJ03
- FEBRA20003990//ZINC FINGER PROTEIN 45 (BRC1744) //4.60E-130//502aa//50%//Q02386
- 55 FEBRA20004040
- FEBRA20004150//DRA PROTEIN (DOWN-REGULATED IN ADENOMA) //2.70E-30//150aa//37%//P40879
- FEBRA20004520
- FEBRA20004540//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1) //2.40E-252//425aa//99%//P51522

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- FEBRA20004910
FEBRA20005360//Homo sapiens paraneoplastic cancer-testis-brain antigen (MA5) mRNA, complete cds.//5.50E-75//375aa//44%//AF083116
- 5 FEBRA20006560
FEBRA20006800
FEBRA20006900
FEBRA20007330//45 KDA CALCIUM-BINDING PROTEIN PRECURSOR (STROMA CELL-DERIVED FACTOR 4) (SDF-4).//3.30E-63//117aa//94%//061112
FEBRA20007400
- 10 FEBRA20007570//Homo sapiens BM-009 mRNA, complete cds.//1.30E-59//189aa//66%//AF208851
FEBRA20007710
FEBRA20007720//Mus musculus strain ICR 90 kDa actin-associated protein palladin mRNA, partial cds.//8.10E-06//144aa//29%//AF205079
FEBRA20007870//Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds.//6.60E-79//144aa//100%//AF017433
- 15 FEBRA20008090
FEBRA20008560//HYPOTHETICAL 40.9 KDA PROTEIN C08B11.5 IN CHROMOSOME II.//4.30E-05//91aa//31%//Q09442 FEBRA20008740
FEBRA20008800//SARCALUMENIN PRECURSOR.//2.10E-07//199aa//30%//P13666 FEBRA20008810//ACTIN 6 (FRAGMENT).//1.00E-103//369aa//50%//P53459
- 20 FEBRA20009010
FEBRA20009590
FEBRA20009720//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.30E-145//514aa//51%//Q96976
FEBRA20010930//MONOCARBOXYLATE TRANSPORTER 4 (MCT 4).//9.00E-22//333aa//28%//I015374
- 25 FEBRA20011330//26S PROTEASOME REGULATORY SUBUNIT S3 (PROTEASOME SUBUNIT P58).//2.10E-54//113aa//100%//I043242
FEBRA20011460//ZINC FINGER PROTEIN 174 (AW-1).//1.90E-12//60aa//55%//Q15697
FEBRA20011970
FEBRA20012270
- 30 FEBRA20012450//NAG14.//4.90E-24//399aa//27%//AF196976
FEBRA20012940
FEBRA20013510
FEBRA20014870
FEBRA20014920//Mus musculus pecanex 1 mRNA, complete cds.//6.50E-120//313aa//72%//AF096286
- 35 FEBRA20015840//DELTA-LIKE PROTEIN PRECURSOR (DLK) (PREAD1POCYTE FACTOR 1) (PREF-1) (ADIPOCYTE DIFFERENTIATION INHIBITOR PROTEIN) [CONTAINS: FETAL ANTIGEN 1 (FA1)].//2.90E-64//323aa//39%//Q09163
FEBRA20015900
FEBRA20015910
- 40 FEBRA20017060//Human APEG-1 mRNA, complete cds.//7.10E-57//113aa//100%//U57099
FEBRA20017150//ZINC-BINDING PROTEIN A33.//4.00E-10//322aa//21%//Q02084 FEBRA20017900//Xenopus laevis RRM-containing protein SEB-4 mRNA, complete cds.//1.20E-79//180aa//88%//AF223427
FEBRA20019890//HYPOTHETICAL PROTEIN KIAA0167.//1.70E-180//339aa//56%//Q99490
FEBRA20020860
- 45 FEBRA20021910
FEBRA20021940
FEBRA20024290
FEBRA20024420//Homo sapiens partial mRNA for choline dehydrogenase (chdh gene).//1.10E-71//143aa//98%//A1272267
- 50 FEBRA20025250//HYPOTHETICAL 73.0 KDA PROTEIN IN CLA4-PUS4 INTERGENIC REGION.//1.40E-09//172aa//29%//P48566
FEBRA20027270
FEBRA20027830
FEBRA20028820
- 55 FEBRA20028970
FEBRA20029080
FEBRA20030540//Halocynthia roretzi mRNA for HrPET-1, complete cds.//2.80E-25//155aa//34%//AB029334
FEBRA20031550

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- FEBRA20033080
FEBRA20034290//RESTIN (CYTOPLASMIC LINKER PROTEIN-170) (CLIP-170) //6.90E-21//87aa//51%//042184
FEBRA20037070
FEBRA20041100//PHOSPHOLIPASE ADRA-B PRECURSOR (EC 3.1.-.-) //1.10E-119//259aa//83%//Q05017
5 FEBRA20041910
FEBRA20042240
FEBRA20042370
FEBRA20042930
FEBRA20043250//Canis familiaris mRNA for C3VS protein //1.90E-191//589aa//66%//X99145
10 FEBRA20043290//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ISOFORM (FRAGMENT) //0//975aa//65%//P29616
FEBRA20044120
FEBRA20044430
FEBRA20044900//Homo sapiens mRNA for CPG2 protein //8.60E-244//509aa//89%//X95466
FEBRA20045920//Homo sapiens mRNA for putative sialoglycoprotease type 2 //5.70E-187//273aa//98%//AJ295148
15 FEBRA20048180//DRR1 PROTEIN (TU3A PROTEIN) //8.80E-58//131aa//87%//095990
FEBRA20050140//ZINC FINGER PROTEIN B4 (ZINC FINGER PROTEIN HPF2) //4.40E-125//505aa//45%//P51523
FEBRA20050790//PROTEIN-TYROSINE PHOSPHATASE STRIATUM-ENRICHED (EC 3.1.3.48) (STEP) (NEURAL-SPECIFIC PROTEIN-TYROSINE PHOSPHATASE) (FRAGMENT) //3.60E-66//149aa//83%//P54829
20 FEBRA20052160//PUTATIVE GLUTAMINE-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1) (NAD(+) SYNTHASE [GLUTAMINE-HYDROLYSING]) //6.60E-33//105aa//64%//P38795
FEBRA20053770
FEBRA20053800//Homo sapiens ubiquitous TPR-motif protein Y isoform (UTY) gene, partial cds; alternatively spliced //3.20E-08//65aa//49%//AF265575
25 FEBRA20054270
FEBRA20057260
FEBRA20057520
FEBRA20057780//INTEGUMENTARY MUCIN A.1 PRECURSOR (FIM-A.1) (PREPROSPASMOLYSIN) //2.40E-07//120aa//27%//P10667
30 FEBRA20057880//LIM domain only 7 isoform c [Homo sapiens] //1.20E-287//545aa//99%//INP_056667
FEBRA20059980
FEBRA20060920//SEGMENT POLARITY PROTEIN DISHEVELLED //6.60E-15//84aa//41%//P51140
FEBRA20061500
FEBRA20062700//PUTATIVE novel haloacid dehalogenase-like hydrolase family protein similar to (archaea) bacterial proteins [Homo sapiens] //0//209aa//100%//CAB43550
35 FEBRA20063150//Homo sapiens topoisomerase II alpha-4 (TOP2A) mRNA, partial cds //8.20E-22//73aa//73%//AF285159
FEBRA20063540
FEBRA20064760//ZINC FINGER PROTEIN 184 (FRAGMENT) //2.10E-182//547aa//54%//Q99676
40 FEBRA20066270
FEBRA20066670
FEBRA20067360//HYPOTHETICAL ZING FINGER PROTEIN KIAA0961 //7.00E-134//472aa//54%//Q9Y2G7
FEBRA20067930//PERSEPHIN PRECURSOR (PSP) //7.90E-23//50aa//100%//060542 FEBRA20068730//Trg protein //1.00E-82//560aa//37%//160486
45 FEBRA20069420//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946) (FRAGMENT) //3.60E-103//284aa//58%//Q06730
FEBRA20070170//Homo sapiens TRAF4-associated factor 2 mRNA, partial cds //1.40E-87//220aa//75%//U83194
FEBRA20072000//MYOSIN II HEAVY CHAIN, NON MUSCLE //3.00E-08//645aa//21%//P08799
FEBRA20072800//Human (c-myc) gene, complete primary cds, and five complete alternatively spliced cds //4.10E-30//97aa//74%//U22376
50 FEBRA20074140
FEBRA20074580
FEBRA20075510//RAS-RELATED PROTEIN RAB-6 //1.00E-36//88aa//88%//P20340
FEBRA20075660//REGU OF MITOTIC SPINDLE ASSEMBLY 1 (RMSA-1) //6.00E-09//84aa//46%//P49646
55 FEBRA20076220
HCASM10000210//Plasmodium berghei strain NYU2 merozoite surface protein-1 mRNA, partial cds //1.50E-08//122aa//28%//AF000413
HCASM10000610//HYPOTHETICAL 63.9 KD PROTEIN C1F12.09 IN CHROMOSOME 1 //2.80E-41//116aa//31%//

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- Q10351
HCASM10001160
HCASM20002020
HCASM20002140//G1/S-SPECIFIC CYCLIN D3.//8.90E-118//226aa//99%//P30281
5 HCASM20003070
HCASM20005340
HCASM20005360//Macrophage migration inhibitory factor//2.50E-17//45aa//100%//XP_000858
HEART20000350//Transacylases//7.50E-35//267aa//35%//RAB94954
HEART20000990
10 HEART20003090//PTB-ASSOCIATED SPLICING FACTOR (PSF)//3.70E-07//143aa//30%//P23246
HEART20004110
HEART20004480//TROPONIN T, CARDIAC MUSCLE ISOFORMS (TNTC)//2.80E-39//81aa//98%//P45379
HEART20004920
HEART20005060//ENAMELIN (TUFTELIN)//1.60E-23//215aa//30%//P27628 HEART20005200//ANKYRIN 1//5.00E-
15 24//250aa//37%//P16157
HEART20005680
HHDPC20000550//ADENYLATE KINASE, CHLOROPLAST (EC 2.7.4.3) (ATP-AMP
TRANSPHOSPHORYLASE)//1.60E-14//201aa//24%//P43188
HHDPC20000950//Cricetulus griseus layilin mRNA, complete cds.//8.00E-177//373aa//84%//AF093673
20 HHDPC20001150//Mus musculus putative secreted protein ZSIG37 (Zsig37) mRNA, complete cds.//2.00E-91//199aa//
83%//AF192499
HHDPC20001490//Mus musculus partial mRNA for muscle protein 534 (mg534 gene)//2.10E-80//167aa//88%//
AJ250189
HHDPC20003150
25 HHDPC20004550//H.sapiens PTPL1 mRNA for protein tyrosine phosphatase//3.60E-32//371aa//26%//X80289
HHDPC20004560
HHDPC20004620
HLUNG10000240
HLUNG10000300
30 HLUNG10000370
HLUNG10000640//KARYOGAMY PROTEIN KAR4//2.20E-27//324aa//27%//P25583
HLUNG10000760//Mus musculus mRNA for mSox7, complete cds.//9.90E-186//388aa//87%//AB023419
HLUNG10000990//TRICHOHYALIN//7.00E-06//454aa//21%//P22793
HLUNG10001050//MYOTUBULARIN//4.60E-12//95aa//37%//Q13496
35 HLUNG10001100//PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP)//6.20E-06//117aa//30%//
Q03211
HLUNG20000680//ZINC FINGER PROTEIN 157//6.30E-104//443aa//45%//P51786 HLUNG20001160//AIG1 PRO-
TEIN//3.10E-24//271aa//28%//P54120
HLUNG20001250
40 HLUNG20001420//Mus musculus putative thymic stromal co-transporter TSCOT mRNA, complete cds.//1.20E-189//
478aa//766//AF148145
HLUNG20001760
HLUNG20002550//MAST CELL TRYPTASE PRECURSOR (EC 3.4.21.59)//1.10E-43//178aa//47%//P50342
45 HLUNG20003140
HLUNG20004120
HLUNG20004800
HLUNG20005010
HSYRA10001190//PROBABLE GYP7 PROTEIN (FRAGMENT)//7.90E-08//157aa//25%//P09379
HSYRA10001370//ZINC FINGER PROTEIN 184 (FRAGMENT)//1.70E-149//556aa//50%//Q99676
50 HSYRA10001480
HSYRA10001680//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III//9.30E-61//540aa//32%//Q09475
HSYRA10001780
HSYRA20001350//CELL POLARITY PROTEIN TEA1//9.10E-16//211aa//28%//P87061
HSYRA20002480
55 HSYRA20002530
HSYRA20003470
HSYRA20005100//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUP-
PRESSOR 1)//6.70E-31//374aa//31%//P30771

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HSYRA20006050//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT) //3.40E-11//282aa//20%//P39922
 HSYRA20006290//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN) //2.10E-07//168aa//30%//
 P17437
 HSYRA20006400//Homo sapiens FRG1 mRNA, complete cds. //1.00E-50//112aa//91%//L76159
 5 HSYRA20007600
 HSYRA20008280
 HSYRA20011030
 HSYRA20011530
 HSYRA2013320//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 3 PRECURSOR (IGFBP-3) (IBP-3)
 10 (IGF-BINDING PROTEIN 3) //1.60E-130//236aa//99%//P17936
 HSYRA20014200
 HSYRA20014760
 HSYRA20015740//GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10) (GLUCOSAMINE-6- PHOSPHATE
 DEAMINASE) (GNPDA) (GLCN6P DEAMINASE) (OSCILLIN) //1.70E-133//274aa//87%//Q64422
 15 HSYRA20015800
 HSYRA20016210
 HSYRA20016310//ZINC FINGER PROTEIN 138 (FRAGMENT) //3.80E-136//237aa//100%//P52744
 IMR3210000440//Human transmembrane receptor precursor (PTK7) mRNA, complete cds. //1.60E-208//388aa//99%//
 U40271
 20 IMR3210000740
 IMR3210000750
 IMR3210001580//Cricetus griseus layilin mRNA, complete cds. //2.30E-177//373aa//84%//AF093673
 IMR3210001650
 IMR3210002420//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946) (FRAG-
 25 MENT). //3. 80E-81//281aa//47%//Q06730
 IMR3210002660//ZINC/CADMIUM RESISTANCE PROTEIN //2.50E-10//148aa//25%//P20107
 IMR3220002230//HINT PROTEIN (PROTEIN KINASE C INHIBITOR 1) (PKCI-1) (17 KD
 INHIBITOR OF PROTEIN KINASE C) //7.90E-08//97aa//82%//P16436
 IMR3220003020//Mus musculus shd mRNA, complete cds. //3.80E-138//337aa//77%//AB018423
 30 IMR3220006090
 IMR3220007420//HYPOTHETICAL ZINC FINGER PROTEIN ZK686.4 IN CHROMOSOME III. //5.50E-50//211aa//
 48%//P34670
 IMR3220007750//FOLLISTATIN-RELATED PROTEIN PRECURSOR (TGF-BETA-INDUCIBLE PROTEIN TSC-36) //
 3.60E-19//229aa//30%//Q62356
 35 IMR3220007910//SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1) //5.00E-07//167aa//31%//P17600
 IMR3220008380//METHIONYL-TRNA FORMYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (EC 2.1.2.9)
 (MTFMT) (FRAGMENT) //1.10E-147//301aa//90%//Q77480
 IMR3220008590
 IMR3220008630//PUTATIVE SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING
 40 FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) //3.50E-05//98aa//40%//Q09511
 IMR3220009190//METHIONINE AMINOPEPTIDASE 2 (EC 3.4.11.18) (METAP 2)
 (PEPTIDASE M 2) (INITIATION FACTOR 2 ASSOCIATED 67 KD GLYCOPROTEIN) (P67) //1.90E-230//418aa//92%//
 Q08663
 IMR3220009350
 45 IMR3220009530
 IMR3220009730//DNA43 PROTEIN //6.20E-13//367aa//23%//P32354
 IMR3220009840
 IMR3220011850
 IMR3220012180//Mus musculus pseudouridine synthase 3 (Pus3) mRNA, complete cds. //3.10E-221//483aa//84%//
 50 AF266505
 IMR3220013170//Homo sapiens mRNA for protein phosphatase, complete cds. //9.10E-41//195aa//48%//AB027004
 IMR3220013320//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M) //5.10E-
 08//357aa//22%//P08553
 IMR3220014350//HYPOTHETICAL PROTEIN KIAA0025 //9.70E-60//408aa//37%//Q15011
 55 IMR3220014910//Rattus norvegicus tricarboxylate carrier-like protein mRNA, complete cds. //3.90E-43//137aa//57%//
 AF276997
 IMR3220016000
 IMR3220017240

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- KIDNE10000080//Xenopus laevis alpha-1 collagen type II mRNA, complete cds //8.60E-07//244aa//29%//M63596
KIDNE10000280
KIDNE10000500
KIDNE10001040//SYNTAXIN 7 //1.10E-32//249aa//32%//O15400
5 KIDNE10001430
KIDNE10001450
KIDNE10001520//Mus musculus yolk sac permease-like molecule 1 (YSPL-1) mRNA, complete cds //6.40E-73//159aa//77%//U25739
KIDNE20000410//ALANINE--GLYOXYLATE AMINOTRANSFERASE 2 PRECURSOR (EC 2.6.1.44) (AGT 2) (BE-TA-ALANINE-PYRUVATE AMINOTRANSFERASE) (BETA-ALAT II) //1.00E-71//167aa//85%//Q64565
10 KIDNE20000510//ZINC FINGER PROTEIN 133 //5.10E-156//503aa//56%//P52736
KIDNE20000700
KIDNE20000850
KIDNE20001670//Mus musculus mRNA for RST, complete cds //6.80E-123//331aa//72%//AB005451
15 KIDNE20001920
KIDNE20002440
KIDNE20002450
KIDNE20002660
KIDNE20003150//AQUAPORIN-7 LIKE (AQUAPORIN ADIPOSE) (AQAP) //1.80E-44//95aa//92%//O14520
20 KIDNE20003300//karos-like protein//1.50E-45//160aa//41%//AAC34387
KIDNE20003490//Mus musculus putative lysophosphatidic acid acyltransferase mRNA, complete cds //6.10E-124//291aa//77%//AF015811
KIDNE20003750//Mus musculus mRNA for granuphilin-a, complete cds //1.30E-31//173aa//42%//AB025258
KIDNE20004030
25 KIDNE20004220//Homo sapiens topoisomerase II alpha-4 (TOP2A) mRNA, partial cds //3.70E-21//76aa//72%//AF285159
KIDNE20004970//TRICHOHYALIN //1.50E-06//244aa//27%//P37709
KIDNE20005100//ALANINE--GLYOXYLATE AMINOTRANSFERASE 2 PRECURSOR (EC 2.6.1.44) (AGT 2) (BE-TA-ALANINE-PYRUVATE AMINOTRANSFERASE) (BETA-ALAT II) //1.30E-153//337aa//84%//Q64565
30 KIDNE20005170//HYPOTHETICAL 49.1 KD PROTEIN C11D3.06 IN CHROMOSOME 1 //2.20E-30//247aa//31%//Q10085
KIDNE20005190//TONB PROTEIN //2.60E-08//93aa//34%//O06432
KIDNE20005740//Staphylococcus epidermidis putative cell-surface adhesin SdrF (sdrF) gene, complete cds //3.10E-34//372aa//28%//AF245041
35 KIDNE20031850//Ras association (RalGDS/AF-6) domain family 2; KIAA0168 gene product [Homo sapiens] //4.00E-66//250aa//59%//NP_055552
KIDNE20033050//PUTATIVE AMIDASE AF1954 (EC 3.5.1.4) //1.30E-34//242aa//32%//O28325
KIDNE20033350
KIDNE20033570
40 KIDNE20033730//Homo sapiens Asef mRNA for APC-stimulated guanine nucleotide exchange factor, complete cds //3.90E-184//572aa//61%//AB042199
KIDNE20033770
KIDNE20033750
KIDNE20039410//HYPOTHETICAL 37.2 KDA PROTEIN C12C2.09C IN CHROMOSOME II //3.20E-19//209aa//22%//Q09749
45 KIDNE20039940//ZINC FINGER PROTEIN 191 //1.40E-82//308aa//56%//O14754
KIDNE20040340
KIDNE20040540
KIDNE20040840//Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds //0//1135aa//64%//AF003249
50 KIDNE20042620
KIDNE20042940
KIDNE20042950//Human mRNA for prepro-alpha2(I) collagen (COL1A2) //1.40E-05//96aa//37%//Y00724
KIDNE20043440//Vacuolar protein sorting-associated protein - fission yeast//9.00E-34//400aa//33%//T39106
55 KIDNE20044110//Homo sapiens vacuolar proton pump 116 kDa accessory subunit (ATP6N1B) mRNA, complete cds, alternatively spliced //3.80E-278//322aa//91%//AF245517
KIDNE20045200
KIDNE20045340

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- KIDNE20045790
KIDNE20046810//Mus musculus peroxisomal long chain acyl-CoA thioesterase lb (Pte1b) gene, exon 3 and complete cds.//2.80E-87//219aa//73%//AF180801
- KIDNE20048280//Mus musculus orphan transporter isoform A12 (Xtrp2) mRNA,
5 alternatively spliced, complete cds.//2.70E-265//600aa//76%//AF075262
- KIDNE20048640
KIDNE20048790
KIDNE20049810
KIDNE20050420//LYSOSOMAL TRAFFICKING REGULATOR (BEIGE HOMOLOG) //5.00E-97//283aa//50%//Q99698
- 10 KIDNE20052960//ACTIN, CYTOPLASMIC 1 (BETA-ACTIN) //2.70E-16//68aa//67%//P12714
- KIDNE20053360//Homo sapiens antigen NY-CO-31 (NY-CO-31) mRNA, partial cds.//6.40E-12//66aa//54%//AF039697
- KIDNE20054000
KIDNE20054720//Drosophila melanogaster minidiscs (mnd) mRNA, complete cds.//4.80E-69//474aa//34%//AF139834
- 15 KIDNE20056290//Bos taurus mRNA for mitochondrial aralkyl acyl-CoA:amino acid N-acyltransferase.//6.40E-58//297aa//40%//AJ223301
- KIDNE20056760//NEURONAL PROTEIN.//6.50E-44//118aa//75%//P41737
- KIDNE20059080//Plakophilin 4 [Homo sapiens] //0//669aa//98%//NP_003619
- KIDNE20059370
20 KIDNE20060140//Rattus norvegicus selective LIM binding factor mRNA, complete cds.//1.30E-255//339aa//94%//AF226993
- KIDNE20060300//Gallus gallus syndesmos mRNA, complete cds.//3.10E-42//149aa//62%//AF095446
- KIDNE20060530//Mus musculus mRNA for acetylglucosaminyltransferase-like protein.//3.70E-252//633aa//69%//AJ006278
- 25 KIDNE20060620
KIDNE20061490//Xenopus laevis RING finger protein mRNA, complete cds.//6.80E-19//136aa//40%//U63817
- KIDNE20062480
KIDNE20062990//B0B1 PROTEIN (BEM1-BINDING PROTEIN) //8.00E-06//332aa//22%//P38041
- KIDNE20063530
30 KIDNE20063760//GAMMA-GLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (EC 3.2.3.2) (GAMMA-GLUTAMYL-TRANSFERASE 1) //7.70E-20//62aa//83%//P19440
- KIDNE20066520
KIDNE20067600//PROSTAGLANDIN F2-ALPHA RECEPTOR REGULATORY PROTEIN PRECURSOR (PROSTAGLANDIN F2-ALPHA RECEPTOR ASSOCIATED PROTEIN) //1.90E-23//293aa//26%//Q62786
- 35 KIDNE20067750//Homo sapiens PTOV1 (PTOV1) gene, complete cds.//7.60E-62//283aa//53%//AF238381
- KIDNE20068800//ACTIN INTERACTING PROTEIN 2 //4.60E-33//143aa//51%//P46681
- KIDNE20070050
KIDNE20070770
KIDNE20071860
- 40 KIDNE20073280//L.mexicana lmsap2 gene for secreted acid phosphatase 2 (SAP2) //3.30E-05//365aa//23%//Z46970
- KIDNE20073520//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) //3.00E-15//536aa//23%//P08640
- KIDNE20073560
KIDNE20074220
- 45 KIDNE20075690//CLAUDIN-10 (OSP LIKE PROTEIN) //8.60E-90//224aa//77%//P78369
- KIDNE20078100//DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (EC 3.6.1.23) (DUTPASE) (DUTP PYROPHOSPHATASE) //7.80E-16//100aa//44%//O41033
- KIDNE20078110//ZING FINGER PROTEIN 202 //3.10E-67//427aa//40%//O95125
- LIVER10000580
50 LIVER10000670//UROCANATE HYDRATASE (EC 4.2.1.49) (UROCANASE) (IMIDAZOLONEPROPIONATE HYDROLASE) //1.50E-87//380aa//35%//P53385
- LIVER10000790//Rattus norvegicus fertility related protein WMP1 mRNA, complete cds.//2.70E-82//254aa//65%//AF094609
- LIVER10000990
55 LIVER10001040//Rattus norvegicus kidney-specific protein (KS) mRNA, complete cds.//6.00E-149//333aa//79%//AF062389
- LIVER10001110
LIVER10001750

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- LIVER10002300//NADH-UBIQUINONE OXIDOREDUCTASE 51 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-51KD) (CI-51KD)//1.80E-99//183aa//100%//P49821
- LIVER10002780
- LIVER10003030
- 5 LIVER10004330//Homo sapiens mRNA for neuropathy target esterase//1.30E-256//710aa//68%//AJ004832
- LIVER10005420//Mus musculus TAGL-alpha mRNA, complete cds//1.20E-204//373aa//76%//AF149837
- LIVER20000330//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN)//1.80E-10//193aa//27%//Q13829
- LIVER20000370//ALPHA-1B-GLYCOPROTEIN//5.00E-159//304aa//96%//P04217
- 10 LIVER20004180
- LIVER20004460
- LIVER20005150
- MAMGL10000320
- MAMGL10000350
- 15 MAMGL10000560
- MAMGL10001780//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 15) (ATP-DEPENDENT RNA HELICASE #46)//2.10E-80//166aa//92%//043143
- MAMGL10001820//SEGMENT POLARITY PROTEIN DISHEVELLED//1.10E-12//84aa//41%//P51140
- MAMGL10001840
- 20 MESAN10000350//MAJOR SURFACE-LABELED TROPHOZOITE ANTIGEN PRECURSOR//2.10E-06//179aa//29%//P21849
- MESAN10001010//Rat trg gene product//6.00E-94//600aa//36%//I60486
- MESAN10001470
- 25 MESAN10001800//BB1=malignant cell expression-enhanced gene/tumor progression-enhanced gene [human, UM-UC-9 bladder carcinoma cell line, mRNA, 1897 nt]//1.60E-162//348aa//87%//S82470
- MESAN20000920//Guanylate kinase-interacting protein 1 Maguin-1, membrane-associated//7.60E-155//477aa//62%//T18293
- MESAN20001490//HYPOTHETICAL 175.8 KD PROTEIN IN GND1-1K1 INTERGENIC REGION//6.70E-163//346aa//58%//P38873
- 30 MESAN20002670
- MESAN20002910//HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21) (HISTIDINE—TRNA LIGASE) (HISRS)//3.60E-98//202aa//96%//P12081
- MESAN20003370
- MESAN20005010//Homo sapiens DNA cytosine methyltransferase 3 alpha (DNMT3A) mRNA, complete cds//6.60E-09//95aa//33%//AF067972
- 35 NB9N41000470//Homo sapiens NY-REN-45 antigen mRNA, complete cds//9.70E-247//250aa//99%//AF155110
- NB9N410001210
- NB9N410001350//RAS-RELATED PROTEIN RAB-1A (YPT1-RELATED PROTEIN)//1.00E-70//109aa//100%//P11476
- 40 NB9N410001460
- NB9N420000420
- NB9N420001040//Mus musculus Shc binding protein (mPAL) mRNA, complete cds//4.40E-286//672aa//77%//AF017152
- NB9N420004950//PROBABLE NUCLEAR ANTIGEN//5.00E-05//246aa//31%//P33485
- 45 NESOP10000870//HOMEBOX PROTEIN SAX-1 (CHOX-3) (FRAGMENT)//1.70E-05//68aa//38%//P19601
- NHNPC10000840//Homo sapiens poly-U binding splicing factor PUF60 (PUF60) mRNA, partial cds//6.80E-196//380aa//99%//AF190744
- NHNPC10001010
- NHNPC10001240//PAIRED MESODERM HOMEBOX PROTEIN 2A (PAIRED-LIKE HOMEBOX 2A) (PHOX2A HOMEODOMAIN PROTEIN)//8.00E-05//109aa//28%//Q62066
- 50 NHNPC2000202060//Bovine viral diarrhoea virus type 2 strain BVDV2-SD1630c polyprotein gene, partial cds//8.70E-77//153aa//92%//AF268178
- NHNPC20002120//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)//2.20E-130//357aa//63%//P51522
- NT2NE10000040
- NT2NE10000140//Schizosaccharomyces pombe caffeine-induced death protein 1 (cid1)mRNA, complete cds//1.00E-31//350aa//29%//AF105076
- 55 NT2NE10000180//SUPPRESSOR PROTEIN SRP40//2.50E-06//219aa//23%//P32563
- NT2NE10000230
- NT2NE10000630//Gallus gallus Dach2 protein (Dach2) mRNA, complete cds//1.90E-147//194aa//78%//AF198349

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NT2NE10000730//RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT (EC 2.5.1.-) (RAB GERANYL-GER-
ANYLTRANSFERASE ALPHA SUBUNIT) (RAB GG TRANSFERASE) (RAB
GGTASE) //3.30E-07//142aa//33%//Q92696

NT2NE10000830//POSSIBLE GUSTATORY RECEPTOR CLONE PTE01 (FRAGMENT) //2.40E-56//182aa//62%//
5 P35894

NT2NE10001200
NT2NE10001630

NT2NE10001850//UDP-N-ACETYLGLUCOSAMINE-PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110
KDA SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT) //6.80E-30//395aa//28%//P56558

10 NT2NE20000380
NT2NE20000560
NT2NE20000640
NT2NE20001740

NT2NE20002140//DUAL SPECIFICITY PROTEIN PHOSPHATASE 8 (EC 3.1.3.48) (EC
3.1.3.16) (NEURONAL TYROSINE THREONINE PHOSPHATASE 1) //1.00E-131//487aa//51%//009112

15 NT2NE20002590//OOCYTE ZINC FINGER PROTEIN XLCOF.1 (FRAGMENT) //6.30E-30//77aa//53%//P18750
NT2NE20002990//69 KD ISLET CELL AUTOANTIGEN (ICA69) (ISLET CELL AUTOANTIGEN 1) //3.30E-113//335aa//
57%//005084

NT2NE20003270//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE)
20 (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) //7.00E-21//739aa//22%//P08640
NT2NE20003690//PROPIONYL-COA CARBOXYLASE ALPHA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PRO-
PANOYL-COA:CARBON DIOXIDE LIGASE) //1.80E-26//68aa//86%//P05165
NT2NE20003840//MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAINS: LINKER HISTONE
PROTEINS ALPHA, BETA, DELTA AND GAMMA] //7.80E-10//366aa//22%//P40631

25 NT2NE20003920
NT2NE20004550//sdk (sidekick) protein //4.90E-11//177aa//31%//T13924
NT2NE20004700
NT2NE20005170//Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds. //1.20E-103//226aa//
90%//AF257737

30 NT2NE20005360//40S RIBOSOMAL PROTEIN SA (P40) (34/67 KD LAMININ RECEPTOR)
(COLON CARCINOMA LAMININ-BINDING PROTEIN) (NEM1CHD4) //1.50E-47//91aa//98%//P08865
NT2NE20005500
NT2NE20005860//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds. //1.70E-85//207aa//
69%//AF023657

35 NT2NE20006360
NT2NE20006580//Homo sapiens mRNA for RET finger protein-like 2 //1.10E-152//288aa//98%//AJ010231
NT2NE20007060
NT2NE20007630
NT2NE20007870

40 NT2NE20008020
NT2NE20008090//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1) //1.90E-207//511aa//71%//
Q03923
NT2NE20009800
NT2NE20011560

45 NT2NE20012470
NT2NE20013240
NT2NE20013370//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds. //4.30E-208//
394aa//97%//AF096870
NT2NE20013640

50 NT2NE20013720//Homo sapiens mRNA for putative ribulose-5-phosphate-epimerase, partial cds. //7.90E-58//116aa//
98%//AJ224326
NT2NE20014030
NT2NE20014280
NT2NE20014350

55 NT2NE20015300
NT2NE20016230
NT2NE20016260//Homo sapiens G-protein coupled receptor RE2 mRNA, complete cds. //2.00E-148//270aa//100%//
AF091890

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- NT2NE20016340//NADH-UBIQUINONE OXIDOREDUCTASE 9 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-9KD) (CI-9KD)//5.50E-26//86aa//68%//P56181
- NT2NE20016480
- 5 NT2NE20016660//PUTATIVE ATP-DEPENDENT RNA HELICASE YDL031W//3.90E-15//176aa//30%//Q12389
- NT2NE20016970//MSF1 PROTEIN//3.00E-23//169aa//34%//P35200
- NT2NE20034080//Rattus norvegicus neurexin alpha mRNA, complete cds.//3.70E-258//449aa//99%//AF086607
- NT2NE20035690//Homo sapiens phosphoinositol 3-phosphate-binding protein-2 (PEPP2) mRNA, complete cds.//1.60E-180//227aa//98%//AF302150
- NT2NE20044900
- 10 NT2NE20047160//Homo sapiens AD-017 protein mRNA, complete cds.//2.70E-91//357aa//47%//AF157318
- NT2NE20053710
- NT2NE20054410//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53)//4.50E-06//121aa//33%//Q15427
- NT2NE20055170//Homo sapiens torsinA (DYT1) mRNA, complete cds.//9.50E-159//232aa//89%//AF007871
- NT2NE20057200//Mus musculus Ubc6p homolog mRNA, complete cds.//3.80E-108//222aa//91%//U93242
- 15 NT2RI10000160
- NT2RI10000270
- NT2RI10000480//Homo sapiens MKP-1 like protein tyrosine phosphatase mRNA, complete cds.//8.30E-49//179aa//50%//AF038844
- NT2RI10001640
- 20 NT2RI20000640
- NT2RI20002700
- NT2RI20002820//NUCLEOLAR AUTOANTIGEN N055.//5.00E-243//437aa//100%//Q92791
- NT2RI20002940
- NT2RI200030410//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6)//9.30E-226//578aa//70%//P28160
- 25 NT2RI20004120//CREB-BINDING PROTEIN//4.40E-05//170aa//30%//Q92793
- NT2RI20004210//ZINC FINGER PROTEIN 75.//1.10E-96//225aa//76%//P51815
- NT2RI20005970
- NT2RI20006690//TRICHOHYALIN.//7.10E-17//222aa//32%//P37709
- NT2RI20006710
- 30 NT2RI20006850//HISTONE H1.2 (H1 VAR. 1) (H1C)//3.30E-05//154aa//25%//P15664
- NT2RI20007380
- NT2RI20008650
- NT2RI20009740
- 35 NT2RI200110100//FATTY ACYL-COA HYDROLASE PRECURSOR, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE B).//1.10E-114//425aa//46%//Q04791
- NT2RI20010830//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)//2.30E-174//554aa//51%//P51523
- NT2RI20010910//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//3.40E-22//195aa//36%//Q08170
- NT2RI20012350
- 40 NT2RI20012440
- NT2RI20013420//Mus musculus cyclin ania-6b mRNA, partial cds.//2.70E-73//163aa//91%//AF211859
- NT2RI20013850//Homo sapiens P38IP (P38IP) mRNA, complete cds.//7.70E-101//213aa//95%//AF093250
- NT2RI20014090//DYSTROPHIN.//3.60E-15//546aa//20%//P11531
- NT2RI20014100
- 45 NT2RI20014490//Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds.//1.30E-263//672aa//73%//AF062476
- NT2RI20014500//TRICHOHYALIN.//4.80E-19//610aa//23%//Q07283
- NT2RI20015190//Homo sapiens misato mRNA, partial cds.//7.60E-149//271aa//100%//AF272833
- NT2RI20015400//Alcohol dehydrogenase/ribitol dehydrogenase//4.30E-107//469aa//44%//AA393456
- 50 NT2RI20015950//Zea mays clone AGP2m1 arabinogalactan protein (agp) mRNA, partial cds.//5.60E-05//180aa//32%//AF134579
- NT2RI20016210//Probable transposase - human transposon MER37//3.50E-19//156aa//35%//S72481
- NT2RI20016570
- NT2RI20017260
- 55 NT2RI20018460//basic domain/leucine zipper transcription factor//3.00E-52//203aa//59%//AAA65688
- NT2RI20018660//Mus musculus erythroid membrane-associated protein ERMAPP (Ermap) mRNA, complete cds.//9.20E-187//385aa//72%//AF153906
- NT2RI20020220//VARIANT-SURFACE-GLYCOPROTEIN PHOSPHOLIPASE C (EC 3.1.4.47) (VSG LIPASE) (GLYC-

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- OSYLPHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (GPI-PLC) //5.60E-21//271aa//27%//015886
 NT2R120020410//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT) //1.20E-05//127aa//32%//P10162
- 5 NT2R120021520
 NT2R120022430
 NT2R120022520
 NT2R120022700//X123 protein//7.20E-80//165aa//97%//168673
 NT2R120025170//Homo sapiens PAR3 (PAR3) mRNA, complete cds //1.30E-113//373aa//45%//AF252293
 NT2R120025300//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) //1.40E-14//628aa//21%//P08640
- 10 NT2R120025410//ZINC FINGER PROTEIN 135 //3.90E-72//301aa//42%//P52742
 NT2R120025540//NUCLEAR AUTOANTIGENIC SPERM PROTEIN (NASP) //1.1E-312//604aa//98%//P49321
 NT2R120025850//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION //1.40E-73//246aa//42%//P39956
- 15 NT2R120026540
 NT2R120028020
 NT2R120028520
 NT2R120029260//ARP2/3 COMPLEX 16 KDA SUBUNIT (P16-ARC) //1.00E-52//154aa//68%//015511
 NT2R120029580//Homo sapiens mRNA for copine VI protein //1.00E-207//425aa//73%//AJ133798
- 20 NT2R120029700
 NT2R120030110//Mus musculus clone:2-65 mRNA, complete cds //2.30E-28//124aa//50%//AB030198
 NT2R120030190
 NT2R120030510
 NT2R120030670
- 25 NT2R120031540//DXS6673E PROTEIN //2.80E-05//240aa//22%//Q14202 NT2R120032050//Homo sapiens transportin2 mRNA, complete cds //0//663aa//98%//AF019039
 NT2R120032220//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01 //4.90E-16//582aa//23%//P25386
 NT2R120033010//Homo sapiens UDP-GlcNAc:alpha-D-mannoside b1,2-N-acetylglucosaminyltransferase 1.2 (MGAT1.2) mRNA, partial cds //1.40E-293//579aa//93%//AF250859
- 30 NT2R120033040
 NT2R120033380
 NT2R120033440//PRESYNAPTIC PROTEIN SAP97 (SYNAPSE-ASSOCIATED PROTEIN 97) (DISCS, LARGE HOMOLOG 1) //2.20E-08//126aa//36%//Q12959
 NT2R120033830//Homo sapiens SGC32445 protein (SGC32445) mRNA, complete cds //1.80E-67//134aa//100%//AF251041
- 35 NT2R120035560
 NT2R120036780//SERINE PROTEASE PC8 PRECURSOR (EC 3.4.21.-) (SUBTILISIN/KEXIN-LIKE PROTEASE PC5) (CONVERTASE PC5) //0//633aa//97%//P41413
 NT2R120036950//TRICHOHYALIN //1.70E-13//313aa//25%//P37709
- 40 NT2R120037510//FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (EC 3.2.2.23) (FAPY-DNA GLYCOSYLASE) //1.20E-05//238aa//28%//P74290
 NT2R120040590
 NT2R120041900//REGULATOR OF MITOTIC SPINDLE ASSEMBLY 1 (RMSA-1) //3.20E-13//108aa//44%//P49646
 NT2R120042840
- 45 NT2R120043040//Homo sapiens NY-REN-2 antigen mRNA, complete cds //2.80E-188//539aa//65%//AF155095
 NT2R120043980
 NT2R120044420
 NT2R120046060
 NT2R120047830
- 50 NT2R120048400
 NT2R120049160
 NT2R120049840
 NT2R120049850
 NT2R120050610
- 55 NT2R120050870//Homo sapiens putative anion transporter 1 mRNA, complete cds //8.10E-262//533aa//96%//AF279265
 NT2R120051500//Mus musculus ST6GalNAc V mRNA for GD1 alpha synthase, complete cds //2.40E-168//336aa//90%//AB030836

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- NT2RI20053350//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/MMS19.1/2.00E-23//234aa//32%/P40469
 NT2RI20053680//Homo sapiens NY-REN-36 antigen mRNA, partial cds.//5.80E-62//124aa//100%/AF155106
 NT2RI20055640//Mus musculus mRNA for ganglioside-induced differentiation associated protein 1.//2.50E-100//319aa//58%/Y17850
 5 NT2RI20056280
 NT2RI20056470//KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4).//2.40E-27B//534aa//99%/P19013
 NT2RI20057230//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//3.00E-28//241aa//36%/Q08170
 10 NT2RI20058110//CELL DIVISION CONTROL PROTEIN 26.//3.30E-18//419aa//25%/P04821
 NT2RI20058510//PLECTIN.//3.50E-07//551aa//21%/P30427
 NT2RI20060710//ZINC FINGER PROTEIN ZIC4 (ZINC FINGER PROTEIN OF THE CEREBELLUM 4).//2.10E-153//312aa//86%/Q61467
 NT2RI20060720//HYPOTHETICAL PROTEIN KIAA0179.//0//692aa//99%/Q14684
 15 NT2RI20061270
 NT2RI20061830//Proline-rich protein M14 precursor//1.50E-17//170aa//37%/A28996
 NT2RI20062100//Mus musculus shd mRNA, complete cds.//1.00E-137//337aa//77%/AB018423
 NT2RI20063450
 NT2RI20064120//Rattus norvegicus mRNA for CDCrel-1A, complete cds.//6.70E-148//280aa//98%/AB027143
 20 NT2RI20064870
 NT2RI20065060//Drosophila melanogaster rudimentary gene, intron 3; anon-15AB gene, complete cds.//1.40E-07//212aa//23%/AF172941
 NT2RI20065530
 NT2RI20066670
 25 NT2RI20066790
 NT2RI20066820//Human WW domain binding protein-1 mRNA, complete cds.//5.70E-46//181aa//46%/U79457
 NT2RI20067030//Homo sapiens nlp mRNA, complete cds.//1.80E-85//406aa//51%/AB017800
 NT2RI20067350//Neofelis nebulosa strain nnex zinc finger protein Zfx (Zfx) gene, partial cds.//2.10E-23//245aa//27%/AF252979
 30 NT2RI20067880
 NT2RI20068250
 NT2RI20068550//Homo sapiens RNA helicase (RIG-I) mRNA, complete cds.//1.20E-52//340aa//34%/AF038963
 NT2RI20070480//Mus musculus DXImx48e protein (DXImx48e) mRNA, complete cds.//3.40E-169//467aa//72%/AF229644
 35 NT2RI20070840
 NT2RI20070960//PROTO-ONCOGENE DBL PRECURSOR [CONTAINS: MCF2].//4.10E-30//431aa//27%/P10911
 NT2RI20071160
 NT2RI20071330//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.80E-240//647aa//64%/Q05481
 40 NT2RI20071480
 NT2RI20072140
 NT2RI20072540//Arabidopsis thaliana ZCF61 mRNA, complete cds.//2.20E-12//113aa//35%/AB028228
 NT2RI20073030
 NT2RI20073840//Homo sapiens mixed lineage kinase mRNA, complete cds.//2.30E-179//362aa//93%/AF238255
 45 NT2RI20073860
 NT2RI20074390//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.30E-97//489aa//41%/P51523
 NT2RI20074690//Homo sapiens NY-REN-58 antigen mRNA, complete cds.//4.00E-221//438aa//99%/AF155115
 NT2RI20074980//Homo sapiens carboxypeptidase Z precursor, mRNA, complete cds.//3.10E-189//357aa//96%/U83411
 50 NT2RI20075070
 NT2RI20075720
 NT2RI20075890
 NT2RI20077230//Homo sapiens BRI3 mRNA, complete cds.//1.80E-114//182aa//99%/AF272043
 NT2RI20077290
 55 NT2RI20077510
 NT2RI20077540//INTESTINAL MEMBRANE A4 PROTEIN (DIFFERENTIATION-DEPENDENT PROTEIN A4) (PROTEOLIPID PROTEIN 2).//2.30E-12//111aa//33%/Q04941
 NT2RI20078270

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- NT2RI20078790//HOMEBOX PROTEIN HOX-A4 (CHOX-1.4)//7.80E-08//83aa//43%//P17277
- NT2RI20078840//ARS BINDING PROTEIN 1 //1.50E-17//313aa//27%//P49777
- NT2RI20078910//DMR-N9 PROTEIN //1.40E-122//398aa//59%//Q08274
- 5 NT2RI20080500//BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC) //5.90E-43//528aa//28%//P98160
- NT2RI20081880//Mus musculus Mporc-b mRNA for porcupine-B, complete cds.//4.40E-64//125aa//97%//AB036746
- NT2RI20082210//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B) //4.70E-12//110aa//37%//Q62267
- NT2RI20083360
- 10 NT2RI20083960//Homo sapiens mRNA for SH3 binding protein, complete cds.//3.60E-31//159aa//44%//AB005047
- NT2RI20084810//1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE ALPHA (EC 2.3.1.51) (1- AGP ACYLTRANSFERASE) (1-AGPAT) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE- ALPHA) (LPAAT-ALPHA) //4.70E-60//114aa//99%//Q99943
- NT2RI20085260
- 15 NT2RI20085980//MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (MGP57/53) (PAS- 6/PAS-7 GLYCOPROTEIN) (MFGM) (SPERM SURFACE PROTEIN SP47) (BP47) (COMPONENTS 15/16) //5.40E-31//174aa//41%//Q95114
- NT2RI20086560
- 20 NT2RI20087140//Homo sapiens PR-domain zinc finger protein 5 (PRDM5) mRNA, complete cds.//6.10E-51//101aa//99%//AF272897
- NT2RI20087490//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53) //2.00E-08//156aa//37%//Q15427
- NT2RI20087910//PROBABLE URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9) (UMP PYRIPHOSPHORYLASE) (UPRTASE) //1.80E-42//159aa//54%//013867
- NT2RI20088010
- 25 NT2RI20088120//AXONEME-ASSOCIATED PROTEIN MST101(2) //4.00E-05//185aa//24%//Q08696
- NT2RI20089420//NEURAL CELL ADHESION MOLECULE L1 PRECURSOR (N-CAM L1) //3.00E-07//104aa//31%//Q05695
- NT2RI20090650//ZINC FINGER PROTEIN 26 (ZFP-26) (MKR3 PROTEIN) (FRAGMENT) //2.10E-30//194aa//37%//P10076
- 30 NT2RI20090860//PLEGTIN //7.20E-14//450aa//24%//P30427
- NT2RI20090830
- NT2RI20091440
- NT2RI20092150//ZINC FINGER PROTEIN 165 //3.10E-46//179aa//56%//P49910
- NT2RI20092890//CARBOXYPEPTIDASE N 83 KD CHAIN (CARBOXYPEPTIDASE N REGULATORY SUBUNIT) (FRAGMENT) //3.70E-29//293aa//31%//P22792
- 35 NT2RI20094060//Homo sapiens rec mRNA, complete cds.//1.40E-112//293aa//62%//AB023584
- NT2RP60000080//Homo sapiens Pig11 (PIG11) mRNA, complete cds.//6.60E-38//117aa//71%//AF010315
- NT2RP60000170
- NT2RP60000320
- 40 NT2RP60000350//Homo sapiens mRNA for SH3 binding protein, complete cds.//1.30E-54//253aa//45%//AB005047
- NT2RP60000390
- NT2RP60000590
- NT2RP60000720//Pinus taeda clone PtaAGP6 putative arabinogalactan protein mRNA, complete cds.//1.50E-05//165aa//29%//AF101785
- 45 NT2RP60000860//Homo sapiens mRNA for NICE-5 protein.//6.30E-192//883bp//99%//AJ243666
- NT2RP60001000//ZINC FINGER PROTEIN 41 (FRAGMENT) //7.10E-128//366aa//59%//P51814
- NT2RP60001090//RING CANAL PROTEIN (KELCH PROTEIN) //6.40E-79//553aa//33%//Q04652
- NT2RP60001230//KINESIN LIGHT CHAIN (KLC) //1.10E-206//566aa//69%//Q07866
- NT2RP60001270//ZINC FINGER PROTEIN ZIC4 (ZINC FINGER PROTEIN OF THE CEREBELLUM 4) //3.70E-131//264aa//67%//Q61467
- 50 NT2RP70000410
- NT2RP70000690//MUCIN 1 PRECURSOR (POLYMORPHIC EPITHELIAL MUCIN) (PEM) (EPISIALIN) (TUMOR-ASSOCIATED MUCIN) (CARCINOMA-ASSOCIATED MUCIN) (TUMOR-ASSOCIATED EPITHELIAL MEMBRANE ANTIGEN) (EMA) (H23AG) (PEANUT- REACTIVE
- 55 NT2RP70000760//TRANSLATION INITIATION FACTOR EIF-2B EPSILON SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR) //1.70E-23//66aa//81%//P47823
- NT2RP70002380//Adiantum capillus-veneris AcExt1 mRNA for Extensin, complete cds.//2.00E-05//93aa//37%//

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- AB008227
NT2RP70002590//HYPOTHETICAL 32.0 KDA PROTEIN IN NN1-STE24 INTERGENIC REGION.//2.20E-12//251aa//28%//P47153
- 5 NT2RP70002710//Mus musculus zinc finger protein 276 C2H2 type (Zfp276) mRNA, complete cds.//1.80E-101//253aa//77%//AF178935
- NT2RP70003640
NT2RP70003910
NT2RP70004250//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMHC-B) //4.30E-08//244aa//24%//P35580
- 10 NT2RP70004770//UDP-N-ACETYLGLUCOSAMINE-PEPTIDE N-AGETYLGLUCOSAMINYLTRANSFERASE 110 KDA SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//1.00E-22//213aa//32%//P56558
- NT2RP70005790
NT2RP70006240//Phosphatidylinositol-4-phosphate 5-kinase homolog T3K9.2//1.90E-16//204aa//30%//T02098
- NT2RP70008120//HOMEOBOX PROTEIN HOX-B9 (HOX-2.5) //2.40E-53//117aa//87%//P20615
- 15 NT2RP70009050//Medicago truncatula mRNA for 85p protein (85p gene) //5.10E-07//229aa//23%//AJ249679
- NT2RP70010800//Mus musculus mRNA for MIL1 (Miw1 like), complete cds.//2.40E-280//614aa//83%//AB032805
- NT2RP70011660//P CATION-TRANSPORTING ATPASE C10C6.6 IN CHROMOSOME IV (EC 3.6.1.-). //0//1165aa//53%//P90747
- NT2RP70012310
20 NT2RP70013050//U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KDA (U1 SNRNP 70 KDA) //1.50E-30//241aa//32%//P09406
- NT2RP70013350
NT2RP70015910//bK57G9.1 (novel Kringle and CUB domain protein) [Homo sapiens].//1.00E-140//247aa//95%//CAB62952
- 25 NT2RP70018560//Mus musculus polyhomeotic (mPh2) mRNA, complete cds.//5.00E-232//465aa//91%//U81491
- NT2RP70021510
NT2RP70022430//Tax1-binding protein TRX - human.//6.00E-71//180aa//93%//S68091
- NT2RP70023760//M PROTEIN, SEROTYPE 2.1 PRECURSOR.//2.20E-13//331aa//25%//P50468
- NT2RP70023790//110 KDA ANTIGEN (PK110) (FRAGMENT) //7.00E-07//162aa//23%//P13813
- 30 NT2RP70024490
NT2RP70024500//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2) //4.80E-66//312aa//38%//P51523
- NT2RP70025540
NT2RP70026190//Mus musculus ubiquitin-protein ligase E3-alpha (Ubr1) mRNA, complete cds.//5.20E-305//597aa//93%//AF061555
- 35 NT2RP70028290//Scm-related gene containing four mbt domains [Mus musculus].//6.00E-59//500aa//31%//NP_062333
- NT2RP70028410
NT2RP70028750//RESTIN (CYTOPLASMIC LINKER PROTEIN-170 ALPHA-2) (CLIP-170) (REED- STERNBERG INTERMEDIATE FILAMENT ASSOCIATED PROTEIN) //2.60E-11//87aa//44%//P30822
- 40 NT2RP70029060//HEAT SHOCK PROTEIN HSP 90-ALPHA (HSP 86) //0//731 aa//99%//P07900
- NT2RP70029820//Homo sapiens GROS1-L protein mRNA, complete cds.//2.40E-177//680aa//51%//AF097432
- NT2RP70030500
NT2RP70030550
45 NT2RP70030910
- NT2RP70032030//ZINC FINGER PROTEIN 184 (FRAGMENT) //3.50E-139//366aa//55%//Q99676
- NT2RP70033040//YceA protein homolog ybfQ - Bacillus subtilis.//1.00E-35//300aa//33%//C69750
- NT2RP70036290//MHG CLASS II TRANSACTIVATOR CiITA //4.80E-09//116aa//31%//P33076
- NT2RP70036320//Microfilarial sheath protein//5.00E-06//92aa//35%//S46966
- 50 NT2RP70036470
NT2RP70036800//RING CANAL PROTEIN (KELCH PROTEIN) //4.50E-107//652aa//38%//Q04652
- NT2RP70039600
NT2RP70040800//CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1) //5.60E-20//307aa//28%//Q06852
- 55 NT2RP70042040//ZINC FINGER PROTEIN MLZ-4 (ZINC FINGER PROTEIN 46) //9.20E-61//254aa//46%//Q03309
- NT2RP70042330//HYPOTHETICAL PROTEIN MJO941 //8.80E-06//133aa//24%//Q57711
- NT2RP70042600//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMHC-B) //4.50E-21//715aa//21%//P35580

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NT2RP70043730
 NT2RP70043960//Mus musculus mRNA for Fish protein.//0//866aa//88%//AJ007012
 NT2RP70045410//Mus musculus MGA protein mRNA, complete cds.//2.70E-265//1040aa//57%//AF205935
 NT2RP70046560//PEREGRIN (BR140 PROTEIN).//1.30E-48//304aa//36%//P55201
 5 NT2RP70046870//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.//9.70E-07//395aa//24%//Q00808
 NT2RP70047510
 NT2RP70047660
 NT2RP70047900
 NT2RP70049150//Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, complete cds.//6.60E-56//209aa//52%//
 10 AB030505
 NT2RP70049250//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//1.90E-08//118aa//33%//P50552
 NT2RP70049750
 NT2RP70052050//Human transformation-related protein mRNA, 3' end.//2.20E-12//74aa//52%//U24521
 NT2RP70052190
 15 NT2RP70054680
 NT2RP70054930
 NT2RP70055020//Homo sapiens mRNA for paraplegin-like protein.//3.00E-29//68aa//94%//Y18314
 NT2RP70055130//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//7.00E-130//461aa//46%//P51523
 NT2RP70055200//INTEGUMENTARY MUCIN A.1 PRECURSOR (FIM-A.1) (PREPROSPASMOLYSIN).//2.40E-07//
 20 120aa//27%//P10667
 NT2RP70061620//ZINC FINGER PROTEIN MFG-3.//3.60E-16//266aa//27%//P16374
 NT2RP70061880//GTPASE-ACTIVATING PROTEIN.//1.70E-08//265aa//21%//P33277
 NT2RP70062960//EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB).//5.80E-67//
 185aa//46%//Q03468
 25 NT2RP70063040//Homo sapiens MLL septin-like fusion protein (MSF) mRNA, complete cds.//1.00E-187//348aa//
 99%//AF123052
 NT2RP70063740
 NT2RP70064080//Drosophila melanogaster F protein (olf186) mRNA, complete cds.//2.50E-54//203aa//56%//
 AF188634
 30 NT2RP70064900//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-149//580aa//40%//P51523
 NT2RP70065270//LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6).//2.40E-136//341aa//61%//U043900
 NT2RP70066210
 NT2RP70067010
 NT2RP70069800
 35 NT2RP70069860//ZINC FINGER PROTEIN 184 (FRAGMENT).//4.40E-141//566aa//46%//Q99676
 NT2RP70071140
 NT2RP70071540
 NT2RP70071770//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//8.50E-
 61//599aa//29%//AF064801
 40 NT2RP70072210//Rattus norvegicus schlafen-4 (SLFN-4) mRNA, complete cds.//1.10E-19//244aa//32%//AF168795
 NT2RP70072520//Human serine/threonine kinase mRNA, partial cds.//1.20E-79//154aa//100%//UJ79240
 NT2RP70073590
 NT2RP70073810//Sulfonylurea receptor 2A.//4.50E-70//135aa//100%//NP_064694
 NT2RP70074060
 45 NT2RP70074220//SYNAPSIN I (BRAIN PROTEIN 4.1).//2.20E-05//116aa//34%//P17600
 NT2RP70075040
 NT2RP70075370//52 KDA RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO (SS-A)).//1.20E-
 97//482aa//42%//P19474
 NT2RP70076100//Homo sapiens mRNA for putative phospholipase, complete cds.//7.10E-189//424aa//53%//
 50 AB019435
 NT2RP70076170
 NT2RP70076430//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4
 SUBUNIT).//1.70E-42//692aa//26%//U060100
 NT2RP70079250//Homo sapiens contactin associated protein (Caspr) mRNA, complete cds.//2.30E-218//963aa//
 55 42%//U87223
 NT2RP70079300
 NT2RP70079750//Homo sapiens BAC526N18 neuexin III gene, partial cds.//5.00E-177//334aa//100%//AF123462
 NT2RP70081330

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- NT2RP70081370//ATP-BINDING CASSETTE, SUB-FAMILY A, MEMBER 1 (ATP-BINDING CASSETTE TRANSPORTER 1) (ATP-BINDING CASSETTE 1) //1.10E-56//364aa//38%/P41233
- NT2RP70081420
- 5 NT2RP70081440//DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 4 (EC 2.7.1.-) (MAP KINASE KINASE 4) (JNK ACTIVATING KINASE 1) (C-JUN N-TERMINAL KINASE KINASE 1) (JNK) (SAPK/ERK KINASE 1) (SEK1) //7.20E-77//162aa//91%/P45985
- NT2RP70081670//85.1 KDA PROTEIN IN GREB-FEOA INTERGENIC REGION //3.10E-108//568aa//38%/P46837
- NT2RP70083150//ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220] //3.60E-09//431aa//23%/P03200
- 10 NT2RP70084060//Probable hexosyltransferase (EC 2.4.1.-) SC2G5.06//4.90E-07//1127aa//32%/T34839
- NT2RP70084410//Polybromo 1 protein - chicken //0//985aa//88%/S60678
- NT2RP70084870//TRICHOYALIN //9.20E-16//452aa//21%/P37709 NT2RP70085500//Mus musculus rig-1 protein mRNA, complete cds //0//976aa//86%/AF060570
- NT2RP70085570//DNA BINDING PROTEIN URE-B1 (EC 6.3.2.-) //3.40E-23//282aa//27%/P51593
- 15 NT2RP70086230
- NT2RP70087200//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2) //1.20E-164//889aa//42%/P51523
- NT2RP70088550//Rattus norvegicus membrane-associated guanylate kinase-interacting protein 2 Maguin-2 mRNA, complete cds //7.90E-267//434aa//98%/AF102854
- NT2RP70090120//CHLORIDE CHANNEL PROTEIN 7 (CLC-7) (FRAGMENT) //0//734aa//99%/P51798
- 20 NT2RP70090190//ZINC FINGER PROTEIN HPF1 (ZINC FINGER PROTEIN HPF1) //3.60E-146//395aa//61%/P51522
- NT2RP70091490//GLUCOSE TRANSPORTER TYPE 2, LIVER //3.30E-17//1109aa//37%/P14246
- NT2RP70091680
- NT2RP70092150
- NT2RP70092360//BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE
- 25 PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC) //4.50E-91//1310aa//26%/Q05793
- NT2RP70092590
- NT2RP70093220//CHLORIDE CHANNEL PROTEIN 5 (CLC-5) //0//746aa//99%/P51795 NT2RP70093630
- NT2RP70093700//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-) //9.90E-11//241aa//21%/P49695
- 30 NT2RP70093730
- NT2RP70093940//Exocyst complex protein sec5 //0//924aa//93%/T09220
- NT2RP70093970
- NT2RP70094290
- NT2RP70094660
- 35 NT2RP70094810//Drosophila melanogaster Dispatched (dispatched) mRNA, complete cds //1.00E-105//579aa//38%/AF200691
- NT2RP70094980//FIBULIN-1, ISOFORM A PRECURSOR //6.50E-30//211aa//38%/P23142
- NT2RP70095020
- NT2RP70095070
- 40 NTONG10000330
- NTONG10000520//Rattus norvegicus mRNA for Kelch related protein 1 (krp1 gene) //2.00E-118//439aa//49%/AJ293948
- NTONG10000980
- NTONG10001230//Mus musculus mRNA, partial cds, clone CLFEST42 //6.10E-07//217aa//25%/D82816
- 45 NTONG10001300//Gallus gallus kinectin mRNA, complete cds //1.30E-15//534aa//22%/J15617
- NTONG10001820//Mus musculus mammalian inositol hexakisphosphate kinase 1 (ip6k1) mRNA, complete cds //5.20E-77//294aa//53%/AF177144
- NTONG10002140//SARCALUMENIN PRECURSOR //3.50E-204//376aa//97%/P13666
- NTONG10002460//CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPENDENT KINASE INHIBITOR P57) (P57KIP2) //1.10E-16//156aa//40%/P49918
- 50 NTONG10002570
- NTONG10002640//HYPOTHETICAL 71.1 KD PROTEIN IN DSK2-CAT8 INTERGENIC REGION //6.90E-98//603aa//39%/Q03262
- NTONG20002650//Probable transmembrane protein of fission yeast //8.50E-63//539aa//28%/T39483
- 55 NTONG20003340//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10) //3.10E-108//225aa//83%/O61967
- NTONG20003630//CREB-BINDING PROTEIN //3.00E-05//160aa//31%/Q92793
- NTONG20004920

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- NTONG20005830
NTONG20008000
NTONG20008780//MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B) //1.40E-42//
330aa//31%//P27790
- 5 NTONG20009660//Mus musculus N-RAP mRNA, complete cds //2.50E-56//393aa//38%//U76618
NTONG20009850
NTONG20011370
NTONG20012220
NTONG20014280
- 10 NTONG20015500//ZINC FINGER PROTEIN 135 //1.40E-128//340aa//64%//P52742 NTONG20016120//Oxystyrol-
binding protein homologue 1 [Mus musculus domesticus] //3.00E-43//342aa//37%//AJ278263
OCBBF10000420
OCBBF10000670
OCBBF10000860
- 15 OCBBF10000910//SORBIN //1.30E-71//145aa//91%//P28220
OCBBF10001040
OCBBF10001180//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN) //
1.00E-12//124aa//37%//Q13829
OCBBF10001190
- 20 OCBBF10001220//RING CANAL PROTEIN (KELCH PROTEIN) //8.50E-32//274aa//31%//Q04652
OCBBF20000130
OCBBF20001280
OCBBF20002310//PHOSPHOLIPASE A2 INHIBITOR SUBUNIT B PRECURSOR (PLI-B) //3.50E-27//307aa//29%//
093233
- 25 OCBBF20002770//EARLY EMBRYOGENESIS ZYG-11 PROTEIN //1.40E-46//348aa//34%//P21541
OCBBF20002870
OCBBF20007190//Putative cleavage and polyadenylation specificity factor [Arabidopsis thaliana] //1.00E-142//450aa//
53%//AAD12712
OCBBF20008240//THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3) (THREONINE-TRNA LIGASE)
30 (THRRS) //1.10E-244//484aa//77%//P26639
OCBBF20009040
OCBBF20009980
OCBBF20010750
- 35 OCBBF20011010//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7) //1.10E-133//405aa//55%//
Q05481
OCBBF20011240//TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSGA) //1.60E-81//391aa//42%//
Q63679
OCBBF20011400//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS8 //3.30E-17//199aa//23%//
P39702
- 40 OCBBF20011760//Mus musculus actin-binding protein (ENC-1) mRNA, complete cds //2.30E-236//527aa//75%//
U65079
OCBBF20012100//Cavia porcellus phosphatidic acid phosphatase 2a (PAP2a) mRNA, complete cds //6.30E-29//
285aa//29%//AF088283
OCBBF20013070
- 45 OGBBF20014020//Mus musculus NSD1 protein mRNA, complete cds //0//886aa//73%//AF064553
OCBBF20014080//H sapiens mRNA for thioesterase 11 //3.00E-67//163aa//83%//X86032
OCBBF20014940//ubiquitin-protein ligase 1 [Arabidopsis thaliana] //2.00E-15//200aa//30%//AAF36454
OCBBF20015270
- 50 OCBBF20015280//MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) //4.90E-23//415aa//22%//
P35748
OCBBF20015860//TRANSCRIPTION ELONGATION FACTOR S-II (TFIIS) //7.70E-06//104aa//33%//P49373
OCBBF20017080
- PANC10000210//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1) (PROLYL 4-HYDROXYLA-
SE BETA SUBUNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (P55) //9.10E-31//231aa//33%//P05307
- 55 PANC10001850
PEBLM10000290
PEBLM10000340//RNA-BINDING PROTEIN EWS //1.80E-284//615aa//83%//Q01844
PEBLM10000680//ACTIN, CYTOPLASMIC TYPE 5 //1.30E-70//158aa//86%//P53505 PEBLM10001440//Trg//2.40E-

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- 212//385aa//60%//GAA48220
PEBLM10001800
PEBLM20000300
PEBLM20001120//Homo sapiens nucleotide-binding site protein 1 mRNA, complete cds.//1.90E-127//899aa//34%//
5 AF298547
PEBLM20001260
PEBLM20001470
PEBLM20002130//Mus musculus genes for integrin α 2M9, hapsin, partial and complete cds.//8.20E-44//246aa//
47%//AB036930
10 PEBLM20002480//ZINC FINGER PROTEIN 157.//8.70E-71//210aa//47%//P51786 PEBLM20002700//Homo sapiens
tissue-type bone marrow zinc finger protein 4 mRNA, complete cds.//6.70E-237//537aa//80%//AF070651
PEBLM20003080//ZINC FINGER PROTEIN 135.//2.40E-133//335aa//65%//P52742
PEBLM20003950//ZINC FINGER PROTEIN 165.//3.20E-35//143aa//59%//P49910
PEBLM20004790//PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN).//4.70E-
15 264//410aa//85%//P39688
PLACE50000370//Homo sapiens mRNA for hVPS11, complete cds.//1.80E-149//281aa//98%//AB027508
PLACE50000580//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//9.60E-76//937aa//
27%//D60100
PLACE50000670
20 PLACE50000680//C4B-BINDING PROTEIN PRECURSOR (C4BP).//5.10E-09//136aa//30%//P08607
PLACE50000800//Human non-lens beta gamma-crystallin like protein (AIM1) mRNA, partial cds.//0//840aa//99%//
U83115
PLACE50001050//Mus musculus mRNA for heparan sulfate 6-sulfotransferase 2, complete cds.//6.10E-236//300aa//
89%//AB024565
25 PLACE50001130//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE)
(1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//2.20E-23//729aa//24%//P08640
PLACE50001530
PLACE50001700//DNAK PROTEIN (HEAT SHOCK PROTEIN 70) (HSP70).//3.00E-05//108aa//30%//Q56235
30 PLACE60000700
PLACE60000800
PLACE60001370
PLACE60002050//TRANSCRIPTIONAL REPRESSOR PROTEIN YY1 (YIN AND YANG 1) (YY-1) (DELTA TRAN-
SCRIPTION FACTOR) (NF-E1).//6.00E-73//212aa//66%//P25490
35 PLACE60002630
PLACE60003710
PLACE60003790//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX
PROTEIN 15) (ATP-DEPENDENT RNA HELICASE #46).//5.30E-104//191aa//99%//O43143
PLACE60004240
40 PLACE60004290
PLACE60005230
PLACE60005500
PLACE60005550//Human (c-myc) gene, complete primary cds, and five complete alternatively spliced cds.//14.60E-
20//71aa//66%//UJ22376
45 PLACE60009530
PLACE60012810//Probable acyl-CoA synthetase (EC 6.2.1.-) - Mycobacterium tuberculosis (strain H37RV).//3.00E-
11//600aa//24%//C70669
PLACE60012940
PLACE60014430//Homo sapiens mRNA for MOCS1A & MOCS1B proteins, complete CDSs.//1.60E-146//283aa//
50 98%//AJ224328
PLACE60018860//ADENYLATE CYCLASE, TYPE IV (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYL CY-
CLASE).//1.30E-244//504aa//90%//P26770
PLACE60019230
PLACE60019250
55 PLACE60020160
PLACE60020840//CYTOCHROME B561 (CYTOCHROME B-561).//1.00E-45//211aa//47%//Q95245
PLACE60021020
PLACE60021510//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.00E-140//351aa//61%//P51523

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- PLACE60024190//TRICHOHYALIN //1.40E-09//299aa//24%//P37709
- PLACE60026680//Homo sapiens Arg/Abi-interacting protein ArgBP2b (ArgBP2b) mRNA, partial cds.//1.00E-254//484aa//96%//AF049885
- PLACE60026920
- 5 PLACE60026990//Human PMS2 related (hPMSR6) mRNA, complete cds.//5.70E-42//112aa//75%//U38980
- PLACE60029490
- PLACE60030380//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2) //3.60E-34//335aa//30%//P51523
- PLACE60030940
- PLACE600310
- 10 PLACE60032040
- PLACE60033720
- PLACE60033990//SPIDROIN 1 (DRAGLINE SILK FIBROIN 1) (FRAGMENT) //1.40E-08//234aa//27%//P19837
- PLACE60037050
- PLACE60037400
- 15 PLACE60037450
- PLACE60038500//Homo sapiens mitochondrial solute carrier mRNA, complete cds.//5.10E-65//171aa//70%//AF155660
- PLACE60040050
- PLACE60043120
- 20 PLACE60043360
- PLACE60043960
- PLACE60043970//Takifugu rubripes retinitis pigmentosa GTPase regulator-like protein gene, partial cds.//2.60E-14//329aa//21%//AF286475
- PLACE60044540//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) //1.90E-46//865aa//26%//P08640
- 25 PLACE60044640//Human placenta (Diff48) mRNA, complete cds.//2.60E-88//414aa//45%//U49187
- PLACE60044910
- PLACE60046630
- PLACE60046870
- 30 PLACE60047380
- PLACE60049310
- PLACE60049930
- PLACE60050290
- PROST10001520
- 35 PROST10001670//SYNAPSIN I (BRAIN PROTEIN 4.1) //2.20E-07//239aa//26%//P17600
- PROST10002200
- PROST10002480
- PROST10002720//Homo sapiens mRNA for calyntenin-2 (CS2 gene) //7.00E-23//153aa//42%//AJ278018
- PROST10003430//Numb-binding protein LNXp80//0//732aa//87%//T09457
- 40 PROST10005260
- PROST10005360//Homo sapiens contactin associated protein (Caspr) mRNA, complete cds.//1.30E-152//719aa//38%//U87223
- PROST10005640
- PROST20000360
- 45 PROST20000530//60S RIBOSOMAL PROTEIN L13A (23 KDA HIGHLY BASIC PROTEIN) //2.00E-33//73aa//95%//P40429
- PROST20001760//RD PROTEIN (WL623) //7.30E-12//104aa//41%//P19426
- PROST20002060
- PROST20002670
- 50 PROST20002730//H4(D10S170) PROTEIN //2.60E-63//118aa//98%//Q16204
- PROST20002740
- PROST20003250//Homo sapiens DAZ associated protein 1 (DAZAP1) mRNA, complete cds.//2.50E-150//264aa//98%//AF181719
- PROST20004630
- 55 PROST20017390
- PROST20017960
- PROST20018230//TRANSCRIPTION FACTOR SP1 //4.60E-59//287aa//42%//Q01714
- PROST20018990//Human Rar protein mRNA, complete cds.//1.20E-127//278aa//88%//U05227

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- PROST20019980
PROST20021620
PROST20023380//Cca3 protein/5.20E-68//142aa//94%//T31081
PROST20025910
5 PROST20026820//DENTIN MATRIX ACIDIC PHOSPHOPROTEIN 1 PRECURSOR (DENTIN MATRIX PROTEIN-1) (DMP-1) (AG1)//6.90E-05//255aa//27%//055188
PROST20028420
PROST20029600//Human butyrophilin (BTF1) mRNA, complete cds.//2.00E-61//144aa//87%//U90543
PROST20031020
10 PROST20031170//DNA BINDING PROTEIN URE-B1 (EC 6.3.2.-)//1.70E-23//282aa//27%//P51593
PROST20032100
PROST20032320//BETA-GLUCURONIDASE PRECURSOR (EC 3.2.1.31) (BETA-G1)//1.20E-18//46aa//91%//P08236
PROST20033020
15 PROST20033030
PROST20033380//KINESIN LIGHT CHAIN (KLC)//7.70E-08//146aa//27%//P46824
PROST20033400//SERINE/THREONINE-PROTEIN KINASE 9 (EC 2.7.1.-)//1.80E-25//65aa//100%//076039
PROST20034720//IMMEDIATE-EARLY PROTEIN//7.80E-11//180aa//24%//Q01042
PROST20037320
20 PROST20039220
PROST20043320//Homo sapiens mRNA for BAP2-beta protein, complete cds.//3.70E-22//431aa//99%//AB015020
PROST20044160//TROPOMYOSIN 5, CYTOSKELETAL TYPE//7.80E-48//100aa//97%//P21107
PROST20044810
PROST20051210//PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (EC 3.1.3.16) (PP2C)//7.00E-16//74aa//41%//P49596
25 PROST20051430
PROST20054260
PROST20056040
PROST20058800
30 PROST20059190//Human breast cancer, estrogen regulated LIV-1 protein (LIV-1) mRNA, partial cds.//1.50E-28//109aa//55%//U41060
PROST20059430
PROST20061960
PROST20062600//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75)//2.20E-07//269aa//22%//Q08170
35 PROST20064500//N-HYDROXYARYLAMINE SULFOTRANSFERASE (EC 2.8.2.-) (HAST-I)//9.10E-38//102aa//70%//P50237
PROST20067370//H. sapiens mRNA for XIAP associated factor-1//2.40E-122//223aa//99%//X99699
PROST20069880//Mus musculus DXImx48e protein (DXImx48e) mRNA, complete cds.//9.6E-31//750aa//79%//AF229644
40 PROST20072370
PROST20072890//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN)//1.50E-11//314aa//70%//Q13829
PROST20073170//Rattus norvegicus zinc finger protein RIN ZF mRNA, complete cds.//1.80E-268//559aa//87%//AF091457
45 PROST20073890//VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF)//5.30E-33//63aa//98%//P15692
PROST20079740//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) (FRAGMENT)//4.10E-09//97aa//36%//P40603
PROST20085160//TROPOMYOSIN, CYTOSKELETAL TYPE (TM30-NM)//2.10E-93//220aa//87%//P12324
50 PROST20094830
PUAEN10000570
PUAEN10000810
PUAEN10001610//GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 1//2.10E-68//448aa//32%//P25655
55 PUAEN10003220
SALGL10000050
SALGL10000470//NG36 [Homo sapiens]//3.00E-53//184aa//96%//AAD21811
SALGL10000650//POLYHOMEOTIC-PROXIMAL CHROMATIN PROTEIN//4.60E-08//71aa//43%//P39769

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- SALGL10001570//APOLIPOPROTEIN L PRECURSOR (APO-L) //5.10E-99//338aa//61%//I014791
 SKMUS10000140//Polyubiquitin 9 - human //2.10E-199//280aa//96%//M26880
 SKMUS10000220//NUCLEAR PORE PROTEIN SEH1 HOMOLOG //2.00E-58//346aa//39%//Q10099
 SKMUS10000640//Mus musculus RING-finger protein MURF mRNA, complete cds //4.10E-111//348aa//60%//
 5 AF294790
 SKMUS10001040//Homo sapiens mRNA for HEXIM1 protein, complete cds //2.40E-49//256aa//47%//AB021179
 SKMUS10001180//Homo sapiens t(3;5)(q25.1;p34) fusion gene NPM-MLF1 mRNA, complete cds //3.60E-126//
 258aa//94%//L49054
 SKMUS10001240
 10 SKMUS10001290//ISOPENTENYL-DIPHOSPHATE DELTA-ISOMERASE (EC 5.3.3.2) (IP ISOMERASE) (ISOPEN-
 TENYL PYROPHOSPHATE ISOMERASE) //4.10E-81//227aa//64%//Q13907
 SKMUS10001770//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA-AS-
 PARTATE METHYLTRANSFERASE) (PMT) (PROTEIN L-ISOASPARTYL
 METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL
 15 METHYLTRANSFERASE) //2.50E-18//213aa//29%//I026915
 SKMUS20000740//Homo sapiens methyltransferase COQ3 (COQ3) mRNA, complete cds //8.50E-166//309aa//99%//
 AF193016
 SKMUS20001170//Homo sapiens MAGEF1 (MAGEF1) mRNA, complete cds //1.50E-74//305aa//50%//AF295378
 SKMUS20002710
 20 SKMUS20003430
 SKMUS20003650//Human (p23) mRNA, complete cds //7.00E-20//110aa//39%//L24804 SKMUS20003900//Homo sa-
 piens 38 kDa Mov34 homolog mRNA, complete cds //1.20E-152//286aa//99%//UJ70734
 SKMUS20004580//Mus musculus N-RAP mRNA, complete cds //4.50E-160//591aa//56%//UJ76618
 SKMUS20004670
 25 SKMUS20004680
 SKMUS20007240//Homo sapiens mRNA for 2-hydroxyphytanoyl-CoA lyase //2.60E-148//318aa//88%//AJ131753
 SKMUS20007740//BALBIAN RING PROTEIN 1 (GIANT SECRETORY PROTEIN I-A) (GSP-IA) (FRAGMENT) //1.
 30E-08//138aa//26%//P02849
 SKMUS20008470
 30 SKMUS20008630//PROBABLE ASPARAGINYL-TRNA SYNTHETASE (EC 6.1.1.22) (ASPARAGINE--TRNA LIGASE)
 (ASNRs) //1.10E-103//445aa//46%//P52276
 SKMUS20009020//BR01 PROTEIN //2.30E-08//232aa//26%//P48582
 SKMUS20009330//RNA polymerase III subunit [Homo sapiens] //1.80E-44//216aa//47%//U93668
 SKMUS20009450
 35 SKMUS20009540//Homo sapiens F-box protein Fbx25 (FBX25) mRNA, partial cds //4.20E-93//263aa//64%//
 AF174605
 SKMUS20010080//Mus musculus mRNA for a skeletal muscle and cardiac protein //1.00E-75//178aa//87%//AJ011118
 SKMUS20011290//NAD-DEPENDENT METHANOL DEHYDROGENASE (EC 1.1.1.244) (MEDH) //3.70E-45//195aa//
 32%//P31005
 40 SKMUS20011470//Mus musculus RP42 mRNA, complete cds //1.30E-32//186aa//36%//AF198092
 SKMUS20013640
 SKMUS20014920//Zinc finger protein //4.40E-05//153aa//24%//T37771
 SKMUS20015010
 SKMUS20015430//Homo sapiens HDCMC29P mRNA, partial cds //3.50E-128//248aa//97%//AF068295
 45 SKMUS20016080
 SKMUS20016310
 SKMUS20016340//HIGH MOBILITY GROUP PROTEIN HM/G2 (HMG 2) //6.00E-11//170aa//25%//P26583
 SKMUS20016620//Oryctolagus cuniculus CARP mRNA, complete cds //2.70E-43//196aa//51%//AF131883
 SKMUS20016680//Neuron-specific signal transduction protein Stac//8.30E-33//218aa//38%//NP_058549
 50 SKMUS20016710
 SKNMC10000070
 SKNMC10000100
 SKNMC10000190
 SKNMC10000290
 55 SKNMC10001100
 SKNMC10001590
 SKNMC10001680
 SKNMC10002290

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- SKNMC10002510//Homo sapiens MT-ABC transporter (MTABC) mRNA, complete cds.//0//672aa//93%//AF076775
- SKNMC10002640
- SKNMC20000650//ZINC FINGER PROTEIN 136.//7.20E-05//311aa//23%//P52737
- SKNMC20000970//M.musculus mRNA for protein Ht9C.//9.80E-22//552aa//75%//U56044
- 5 SKNMG20002240//ZINC FINGER PROTEIN 228.//1.80E-68//226aa//53%//Q9UJU3
- SKNMC20003050
- SKNMC20003220//MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B) //3.70E-10//153aa//32%//P07199
- SKNMC20003560//Mus musculus Max-interacting transcriptional repressor (Mad3) mRNA, complete cds.//1.90E-72//168aa//86%//U32394
- 10 SKNMC20005930
- SKNMC20006120
- SKNMC20010570
- SKNMC20011130//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//6.90E-90//244aa//86%//AF015264
- 15 SKNMC200015030//P-SELECTIN GLYCOPROTEIN LIGAND 1 PRECURSOR (PSGL-1) (SELECTIN P LIGAND).//3.60E-11//152aa//32%//Q62170
- SKNMC20015550
- SKNMC20015960//Homo sapiens mRNA for ANKHZN, complete cds.//0//1046aa//95%//AB037360
- 20 SKNSH10000860
- SKNSH10001740//ORNITHINE DECARBOXYLASE (EC 4.1.1.17) (ODC).//9.00E-102//352aa//53%//P00860
- SKNSH10003010//Homo sapiens DRC3 mRNA, complete cds.//3.00E-154//305aa//91%//AF282167
- SKNSH10003080
- SKNSH20001510
- 25 SKNSH20001830
- SKNSH20003470//CYTOCHROME B2 PRECURSOR (EC 1.1.2.3) (L-LACTATE DEHYDROGENASE (CYTOCHROME)) (L-LACTATE FERRICYTOCHROME C OXIDOREDUCTASE) (L-LCR).//2.60E-07//107aa//32%//P00175
- SMINT10000160//2-HYDROXYACYLSPHINGOSINE 1-BETA-GALACTOSYLTRANSFERASE PRECURSOR (EC 2.4.1.45) (UDP-GALACTOSE-CERAMIDE GALACTOSYLTRANSFERASE) (CERAMIDE UDP-GALACTOSYLTRANSFERASE) (CEREBROSIDE SYNTHASE).//3.80E-71//492aa//33%//064676
- 30 SMINT10000390
- SMINT10000420//ATP-BINDING CASSETTE, SUB-FAMILY A, MEMBER 3 (ATP-BINDING CASSETTE TRANSPORTER 3) (ATP-BINDING CASSETTE 3) (ABC-C TRANSPORTER).//2.70E-92//662aa//34%//099758
- 35 SMINT10000540
- SMINT10000570//Homo sapiens leucocyte immunoglobulin-like receptor-8 (LIR-8) mRNA, complete cds.//5.30E-212//481aa//84%//AF025534
- SMINT10000710
- SMINT10001000//PAIRED MESODERM HOMEOBOX PROTEIN 2B (PAIRED-LIKE HOMEOBOX 2B) (PHOX2B HOMEODOMAIN PROTEIN) (NEUROBLASTOMA PHOX) (NBPHOX).//1.60E-05//87aa//39%//Q99453
- 40 SMINT10001030//Homo sapiens ankyrin repeat-containing protein ASB-2 mRNA, complete cds.//1.20E-292//546aa//99%//AF159164
- SMINT10001180
- SMINT20000190
- 45 SMINT20000400
- SMINT20001450//Halocynthia roretzi mRNA for HrPET-3, complete cds.//2.30E-20//125aa//40%//AB029335
- SMINT20002270
- SMINT20002390
- SMINT20002770//BUTYROPHILIN PRECURSOR (BT).//3.20E-51//269aa//41%//P18892
- 50 SMINT20003960//A kinase anchor protein AKAP-KL isoform 2.//5.00E-254//738aa//70%//T09226
- SMINT20004000//Homo sapiens FRG1 mRNA, complete cds.//7.00E-52//116aa//90%//L76159
- SMINT20005450//Mus musculus Zfp228 (Znf228) mRNA, complete cds.//1.20E-31//125aa//49%//AF282919
- SMINT20005580
- SPLN10000490
- 55 SPLN10000910//Homo sapiens HRIHFB2007 mRNA, partial cds.//5.20E-95//199aa//90%//AB015330
- SPLN10001430//HIGH MOBILITY GROUP PROTEIN HMG1 (HMG-1).//3.00E-78//147aa//100%//P09429
- SPLN20000200//Human (c-myb) gene, complete primary cds, and five complete alternatively spliced cds.//3.10E-11//644aa//57%//U22376

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SPLN20000470
 SPLN20000720//ZINC FINGER PROTEIN CKR1.//3.10E-37//235aa//37%//P30373
 SPLN20001340//CARBOXYPEPTIDASE S PRECURSOR (EC 3.4.17.4) (YSCS) (GLY-X CARBOXYPEPTIDASE).//
 3.30E-29//250aa//37%//P27614
 5 SPLN20001970//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//
 2.70E-14//243aa//28%//Q08170
 SPLN20002420
 SPLN20002430
 SPLN20002670//Rattus norvegicus TGF-beta resistance-associated protein (TRAG) mRNA, complete cds.//0//
 10 559aa//84%//AF305813
 SPLN20002700
 SPLN20003100
 SPLN20003570//Mus musculus RaiGDS-like protein 3 mRNA, complete cds.//8.30E-191//453aa//81%//AF237669
 SPLN20004430
 15 SPLN20004960
 SPLN20005410
 STOMA10000470
 STOMA10000520
 STOMA10001170
 20 STOMA10001330
 STOMA10001860//CYTOSOLIC ACYL COENZYME A THIOESTER HYDROLASE (EC 3.1.2.2)
 (LONG CHAIN ACYL-COA THIOESTER HYDROLASE) (CTE-II).//2.70E-173//328aa//99%//000154
 STOMA20000320
 STOMA20000880//IG LAMBDA CHAIN C REGIONS.//1.50E-51//105aa//96%//P01842
 25 STOMA20001210//Fugu rubripes CCLB1 gene, exons 1 to 12.//1.90E-127//415aa//55%//Y17462
 STOMA20001880
 STOMA20002570
 STOMA20002890
 STOMA20003960//LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6).//3.60E-59//352aa//39%//043900
 30 STOMA20004780
 STOMA20004820//1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) delta-2//6.90E-148//
 325aa//84%//S14113
 SYNOV10001280//Homo sapiens colon cancer-associated protein Mic1 (MIC1) mRNA, complete cds.//1.1E-316//
 609aa//97%//AF143536
 35 SYNOV10001540
 SYNOV20001770
 SYNOV20002910//Arabinogalactan-like protein//2.90E-07//124aa//31%//S52994
 SYNOV20008200//Trichoplusia ni transposon IFP2.//4.10E-13//254aa//27%//J04364 SYNOV20010140//Mus muscu-
 lus Zfp228 (Znf228) mRNA, complete cds.//2.50E-31//125aa//49%//AF282919
 40 SYNOV20011440
 SYNOV20013740//ZINC FINGER PROTEIN 134.//1.80E-108//332aa//53%//P52741
 SYNOV20014510//MYOCYTE-SPECIFIC ENHANCER FACTOR 2B (SERUM RESPONSE FACTOR-LIKE PROTEIN
 2) (XMEF2) (RSRFR2).//6.40E-140//302aa//88%//Q02080
 SYNOV20014570
 45 SYNOV20016480//THYMIDINE PHOSPHORYLASE PRECURSOR (EC 2.4.2.4) (TDRPASE) (TP) (PLATELET-DE-
 RIVED ENDOTHELIAL CELL GROWTH FACTOR) (PD-ECGF) (GLIOSTATIN).//2.80E-35//69aa//100%//P19971
 TEST110000230
 TEST110000250//M.musculus mRNA for testis-specific protein, DDC8.//2.60E-68//462aa//42%//Y09878
 TEST110000420//PARAMYOSIN (ANTIGEN SJ97).//2.50E-08//367aa//23%//Q05870
 50 TEST110000510//CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 2 (CYTADHERENCE ACCESSORY
 PROTEIN 2).//4.00E-13//648aa//22%//P75471
 TEST110000550//HOMEBOX PROTEIN SIX1 (FRAGMENT).//8.90E-11//199aa//30%//Q62231
 TEST110000640//Fugu rubripes sex comb on midleg-like 2 protein (SCML2) gene, complete cds.//2.20E-140//513aa//
 49%//AF146688
 55 TEST110000700//Rattus norvegicus deubiquitinating enzyme Ubp69 (ubp69) mRNA, complete cds.//7.00E-297//
 618aa//88%//AF106659
 TEST110000960
 TEST110001250

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- TEST10001270//POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE PROTEIN 1)//3.60E-11//161aa//33%//P98161
- TEST10001310//Homo sapiens TCP11 (TCP11) mRNA, complete cds.//1.90E-223//425aa//100%//AF269223
- TEST10001380//NEUROENDOCRINE CONVERTASE 3 PRECURSOR (EC 3.4.21.61) (NEC 3) (PC4) (PROHORMONE CONVERTASE 3) (KEX2-LIKE ENDOPROTEASE 3)//1.10E-140//303aa//85%//P29121
- TEST10001630
- TEST10001680//PROTEIN PHOSPHATASES PP1 REGULATORY SUBUNIT SDS22//4.30E-14//158aa//35%//P36047
- TEST10001790
- TEST10001910//Homo sapiens 88-kDa Golgi protein (GM88) mRNA, complete cds.//8.70E-77//274aa//59%//AF204231
- TEST120000180
- TEST120000440//TRICHOHYALIN//3.00E-16//476aa//26%//P22793
- TEST120001200//Homo sapiens mRNA for zinc finger 3 (ZF3 gene)//6.90E-13//108aa//40%//X60153
- TEST120001540//PUTATIVE SERINE/THREONINE-PROTEIN KINASE D1044.3 IN CHROMOSOME III (EC 2.7.1.-)//1.30E-32//103aa//48%//P41951
- TEST120001770//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3) (SERUM-DERIVED HYALURONAN-ASSOCIATED PROTEIN) (SHAP)//6.10E-05//157aa//22%//Q06033
- TEST120001790
- TEST120001840//SIT4-ASSOCIATING PROTEIN SAP185//7.90E-08//109aa//33%//P40856
- TEST120002070//NIFU-LIKE PROTEIN//3.60E-43//105aa//80%//Q9ZD61
- TEST120002080//Homo sapiens mRNA for Gab2, complete cds.//7.60E-62//222aa//60%//AB018413
- TEST120002380
- TEST120002530//Homo sapiens A1U mRNA, complete cds.//6.60E-17//220aa//31%//AF188240
- TEST120003560//TUBULIN ALPHA-3/ALPHA-7 CHAIN//2.00E-40//119aa//73%//P05214
- TEST120003720
- TEST120004350//CALDESMON (CDM)//1.20E-09//180aa//23%//P12957
- TEST120004620
- TEST120005200
- TEST120005910//ADENYLATE KINASE, CHLOROPLAST (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE)//3.60E-34//209aa//37%//P43188
- TEST120006000//RESTIN (CYTOPLASMIC LINKER PROTEIN-170 ALPHA-2) (CLIP-170) (REED- STERNBERG INTERMEDIATE FILAMENT ASSOCIATED PROTEIN)//6.80E-21//196aa//32%//P30622
- TEST120006270
- TEST120006710
- TEST120006950//KINESIN HEAVY CHAIN//7.80E-07//391aa//22%//P21613
- TEST120006990//KINESIN-LIKE PROTEIN KIF2 (KINESIN-2) (HK2)//2.00E-184//539aa//63%//J000139
- TEST120007070//DOUBLESEX PROTEIN, MALE-SPECIFIC//3.00E-13//163aa//31%//P23023
- TEST120007620//DRA PROTEIN (DOWN-REGULATED IN ADENOMA)//1.60E-09//88aa//38%//P40879
- TEST120007840//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT)//6.00E-89//1092aa//26%//O60100
- TEST120008190
- TEST120008300
- TEST120008490//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT)//4.90E-09//331aa//24%//P39922
- TEST120008830//MYOSIN-BINDING PROTEIN C, SLOW-TYPE (SLOW MYBP-C) (C-PROTEIN, SKELETAL MUSCLE SLOW-ISOFORM)//4.20E-88//162aa//100%//Q00872
- TEST120009090
- TEST120009510
- TEST120009700
- TEST120010080
- TEST120010490//HYPOTHETICAL ZINC FINGER PROTEIN KIAA0961//2.70E-155//504aa//56%//Q9Y2G7
- TEST120010820
- TEST120011340
- TEST120011410//Rattus norvegicus actin-filament binding protein Frabin mRNA, complete cds.//0//766aa//83%//AF038388
- TEST120011800//TRICHOXYALIN//5.80E-07//322aa//22%//Q07283
- TEST120012370//RING CANAL PROTEIN (KELCH PROTEIN)//1.60E-38//438aa//26%//Q04652

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- TESTI20012690//DIHYDROLIPOAMIDE ACETYLTRANSFERASE COMPONENT OF PYRUVATE
DEHYDROGENASE COMPLEX, MITOCHONDRIAL PRECURSOR (EC 2.3.1.12) (E2) (PDC-E2) (70 KDA MITO-
CHONDRIAL AUTOANTIGEN OF PRIMARY BILIARY CIRRHOSIS) (PBC) (M2
ANTIGEN COMPLEX 70 KDA SUBUNIT) //3.40E-308//575aa//99%//P10515
- 5 TESTI20013060
TESTI20013300//Homo sapiens NY-REN-60 antigen mRNA, partial cds.//1.10E-172//315aa//99%//AF155116
TESTI20013450//M.musculus Tenr mRNA for RNA binding protein //3.00E-273//576aa//88%//X84693
TESTI20013520
TESTI20014120//TRICHOHYALIN //1.40E-28//370aa//27%//P37709
- 10 TESTI20014200//D.melanogaster mRNA for putative organic cation transporter,
2064 bp //4.20E-54//357aa//33%//Y12400
TESTI20015110//MYOSIN II HEAVY CHAIN, NON MUSCLE //3.50E-07//255aa//24%//P08799
TESTI20015120//TOM1 (target of myb 1) //1.00E-57//245aa//56%//NP_005479
TESTI20015560//ZING FINGER PROTEIN 151 (MYC-INTERACTING ZINC FINGER PROTEIN) (MIZ-1 PROTEIN) //
- 15 9.50E-16//278aa//28%//Q13105
TESTI20015930
TESTI20016210
TESTI20016610//DYNEIN BETA CHAIN, FLAGELLAR OUTER ARM.//1.10E-17//432aa//25%//Q39565
TESTI20016650//IMMEDIATE-EARLY PROTEIN //9.50E-06//111aa//28%//Q01042
- 20 TESTI20016710
TESTI20017580
TESTI20017660
TESTI20017920
TESTI20018150//GASTRULA ZINC FINGER PROTEIN XLGCF7.1 (FRAGMENT) //7.20E-13//98aa//37%//P18735
- 25 TESTI20018260
TESTI20018270//TRANSETOLASE (EC 2.2.1.1) (TK) (P68) //6.90E-230//614aa//67%//P40142
TESTI20018290
TESTI20018520//Homo sapiens contactin associated protein (Caspr) mRNA, complete cds.//5.40E-167//724aa//40%//
U87223
- 30 TESTI20018620
TESTI20018690//Xenopus laevis bicaudal-C (Bic-C) mRNA, complete cds.//1.20E-08//189aa//30%//AF224746
TESTI20018790//ZINC FINGER PROTEIN 157 //8.70E-104//443aa//45%//P51786
TESTI20018980
TESTI20019500
- 35 TESTI20019680
TESTI20019910
TESTI20020020
TESTI20020480
TESTI20020570//Human actin-like peptide mRNA, partial cds.//6.10E-140//307aa//88%//U20582
- 40 TESTI20020810//HYPOTHETICAL 80.0 KDA PROTEIN IN POLI-RAS2 INTERGENIC REGION //5.30E-40//235aa//
35%//P50944
TESTI20020900
TESTI20021050//MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAINS: LINKER HISTONE
PROTEINS ALPHA, BETA, DELTA AND GAMMA] //3.90E-11//365aa//24%//P40631
- 45 TESTI20021490//ZINC FINGER PROTEIN 131 (FRAGMENT) //5.30E-191//347aa//99%//P52739
TESTI20022230//Chlamydomonas reinhardtii strain 1132D- flagellar
protofilament ribbon protein (RIB43a) mRNA, complete cds.//7.70E-12//137aa//31%//AF196576
TESTI20022450
TESTI20022510
- 50 TESTI20022560//GUANYLATE KINASE (EC 2.7.4.8) (GMP KINASE) //2.20E-20//188aa//31%//Q64520
TESTI20022640
TESTI20022940//MOB2 PROTEIN (MPS1 BINDER 2) //4.80E-16//133aa//31%//P43563
TESTI20023610
TESTI20023690
- 55 TESTI20024150
TESTI20024230//PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR
(PELP) //8.40E-15//155aa//34%//Q03211
TESTI20024610//TRICHOHYALIN //3.60E-13//423aa//23%//P37709

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TESTI20024650//FIBROIN HEAVY CHAIN PRECURSOR (FIB-H) (FRAGMENTS) //4.70E-06//142aa//33%//P05790
 TESTI20024670
 TESTI20024980//Danio rerio p55-related MAGUK protein DLG3 (dlg3) mRNA, complete cds. //2.00E-221//532aa//
 75%//AF124435
 5 TESTI20025160//MELANOMA-ASSOCIATED ANTIGEN B1 (MAGE-B1 ANTIGEN) (MAGE-XP ANTIGEN) (DAM10).
 //1.40E-89//349aa//54%//P43366
 TESTI20025440
 TESTI20025800
 TESTI20026320
 10 TESTI20026760//ZINC-BINDING PROTEIN A33 //1.60E-38//235aa//37%//Q02084
 TESTI20026980
 TESTI20027000
 TESTI20027070//PLASMA-CELL MEMBRANE GLYCOPROTEIN PC-1 [INCLUDES: ALKALINE
 PHOSPHODIESTERASE I (EC 3.1.4.1); NUCLEOTIDE PYROPHOSPHATASE (EC 3.6.1.9) (NPPASE)] //1.50E-50//
 15 406aa//33%//P22413
 TESTI20027290//Homo sapiens mRNA for oligophrenin 1 //2.50E-56//393aa//38%//AJ001189
 TESTI20027890//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN K0X31) (KIA0065) (HA0946) (FRAG-
 MENT) //9.40E-91//472aa//42%//006730
 TESTI20028060
 20 TESTI20028400
 TESTI20028660
 TESTI20029120//DUAL-SPECIFICITY TYROSINE-(Y)-PHOSPHORYLATION REGULATED KINASE (EC 2.7.1.-)
 (PROTEIN KINASE MINIBRAIN HOMOLOG) (HP86) //1.90E-47//253aa//41%//Q13627
 TESTI20029650
 25 TESTI20030050//Mus musculus taube nuss mRNA, complete cds. //1.70E-119//260aa//91%//AF222802
 TESTI20030370
 TESTI20030590//TESTIS-SPECIFIC PROTEIN PBS13 //1.70E-33//117aa//61%//Q01755
 TESTI20030710//Homo sapiens C2H2 (Kruppel-type) zinc finger protein mRNA,
 complete cds //9.80E-18//139aa//46%//AF159567
 30 TESTI20030740//TRICHOHYALIN //8.30E-12//368aa//24%//P22793
 TESTI20031090//VACUOLAR PROTEIN 8 //3.80E-23//367aa//27%//P39968
 TESTI20031170//Tekin A1 [Strongylocentrotus purpuratus] //3.40E-91//397aa//45%//M97188
 TESTI20031300
 TESTI20031520
 35 TESTI20031930
 TESTI20031960
 TESTI20032280
 TESTI20032650
 TESTI20032800
 40 TESTI20032990
 TESTI20033250//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE
 P-F] (FRAGMENT) //4.50E-05//138aa//28%//P02812
 TESTI20033270//Testis-specific protein [Homo sapiens] //1.00E-22//120aa//47%//NP_067063 TESTI20033540//TRI-
 CHOYALIN //1.80E-13//443aa//22%//P37709
 45 TESTI20033560
 TESTI20033760
 TESTI20034130//Zinc finger protein 106 //9.30E-263//781aa//66%//T14273
 TESTI20034180
 TESTI20034190//Homo sapiens very long-chain acyl-CoA synthetase (BG1) mRNA, complete cds. //3.00E-131//
 50 468aa//53%//AF179481
 TESTI20034980//TRIPLE FUNCTIONAL DOMAIN PROTEIN //1.00E-77//250aa//55%//U75962
 TESTI20035120//SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN) //9.30E-06//459aa//20%//062209
 TESTI20035410
 TESTI20035510//Proliferating-cell nucleolar antigen P120-like protein - Archaeoglobus fulgidus //3.00E-12//200aa//
 55 35%//F69504
 TESTI20035740//A-KINASE ANCHOR PROTEIN 150 (AKAP 150) (CAMP-DEPENDENT PROTEIN KINASE REGU-
 LATORY SUBUNIT II HIGH AFFINITY BINDING PROTEIN) (P150) (FRAGMENT) //4.50E-09//357aa//21%//P24587
 TESTI20035800

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- TESTI20035890
 TESTI20036250//IMMEDIATE-EARLY PROTEIN.//1.60E-07//120aa//35%//Q01042
 TESTI20036490//GLYCOPROTEIN X PRECURSOR.//7.40E-06//107aa//31%//P28968
 TESTI20037270
 5 TESTI20037810
 TESTI20038940
 TESTI20039140//Tektin A1//2.10E-66//410aa//36%//A46170
 TESTI20039980//T-CELL RECEPTOR BETA CHAIN ANA 11.//4.40E-13//123aa//40%//P06333
 TESTI20040000//Rattus norvegicus cca2 mRNA, complete cds.//5.60E-82//179aa//86%//AB00199
 10 TESTI20040310
 TESTI20041110
 TESTI20041220//Babesia bigemina 200 kDa antigen p200 mRNA, partial cds.//4.60E-05//481aa//19%//AF142406
 TESTI20042070//Columba livia mRNA for 5'-nucleotidase.//8.20E-113//317aa//67%//AJ131243
 TESTI20042290//MHC CLASS II TRANSACTIVATOR GIITA.//6.30E-05//89aa//43%//P79621
 15 TESTI20042430
 TESTI20042870//X INACTIVE SPECIFIC TRANSCRIPT PROTEIN (FRAGMENT).//2.40E-06//155aa//32%//P27571
 TESTI20042950//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE)
 (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//4.40E-19//141aa//33%//009175
 TESTI20047120//POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE IK (EC 3.6.1.-) (FRAGMENT).//1.00E-
 20 86//169aa//98%//060423
 TESTI20049290
 TESTI20049820//CGMP-DEPENDENT PROTEIN KINASE 1, ALPHA ISOZYME (EC 2.7.1.37) (CGK 1 ALPHA) (CG-
 KI-ALPHA).//6.60E-07//187aa//26%//Q13976
 TESTI20049940
 25 TESTI20051550
 TESTI20052680//Rattus norvegicus RSD-6 mRNA, complete cds.//4.20E-61//261aa//55%//AF271155
 TESTI20053960//ZINC FINGER PROTEIN 132.//0//589aa//99%//P52740
 TESTI20054080//SER/THR-RICH PROTEIN T10 IN DGCR REGION.//4.90E-117//263aa//82%//P54797
 TESTI20054920
 30 TESTI20055840//Homo sapiens Tandem PH Domain Containing Protein-1 mRNA, complete cds.//2.70E-162//331aa//
 92%//AF286160
 TESTI20056900//ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPRO-
 TEIN GP220].//1.50E-06//171aa//32%//P03200
 TESTI20057310//CHROMOSOME SCAFFOLD PROTEIN SCIL.//1.90E-05//297aa//20%//Q90988
 35 TESTI20057420//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED
 DIAZEPAM BINDING INHIBITOR) (MA-DBI).//5.20E-225//501aa//83%//P07106
 TESTI20058600//MYELOID UPREGULATED PROTEIN.//2.20E-68//167aa//74%//035682
 TESTI20062380
 TESTI20062550
 40 TESTI20064250
 TESTI20064830//Homo sapiens RAN binding protein 16 mRNA, complete cds.//5.00E-163//414aa//64%//AF064729
 TESTI20065720//PROTEIN D52 (N8 PROTEIN).//1.00E-22//129aa//46%//P55327
 TESTI20067740
 TESTI20068660//Homo sapiens infertility-related sperm protein mRNA, complete cds.//5.90E-197//365aa//99%//
 45 AF311312
 TESTI20068720
 TESTI20069780
 TESTI20069790
 TESTI20071830//Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds.//1.40E-125//
 50 233aa//99%//AF119043
 TESTI20073580
 TESTI20074020
 TESTI20074640//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//3.20E-119//428aa//45%//
 Q03923
 55 TESTI20074660//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.30E-194//509aa//68%//
 Q05481
 TESTI20074800
 TESTI20076130

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TESTI20077490
 TESTI20077500
 TESTI20078140//D7 PROTEIN //1.10E-25//99aa//49%//P13007
 TESTI20078640//Homo sapiens zinc finger protein ZNF232, exon 4 and complete cds.//2.60E-61//119aa//99%//
 5 AF080171
 TESTI20078670//RING CANAL PROTEIN (KELCH PROTEIN)//8.90E-09//269aa//20%//Q04652
 TESTI20078720//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01 //2.90E-17//417aa//24%//P25386
 TESTI20079510//NEURAL CELL ADHESION MOLECULE, 140 KDA ISOFORM PRECURSOR (N-CAM 140) (NCAM-
 140) (CD56 ANTIGEN)//0//723aa//96%//P13591 TESTI20080200//DPY-19 PROTEIN //7.50E-114//621aa//38%//
 10 P34413
 TESTI20080330
 TESTI20081390
 TESTI20081440
 TESTI20082340
 15 TESTI20082400
 TESTI20083430
 TESTI20083870//CALCINEURIN B-LIKE PROTEIN (CBLP) //1.80E-73//169aa//82%//P28470
 TESTI20084400
 TESTI20086570//MELANOMA-ASSOCIATED ANTIGEN B4 (MAGE-B4 ANTIGEN) //4.20E-88//347aa//52%//015481
 20 TESTI20087740
 TESTI20088470
 TESTI20136910
 TESTI20138320//Xenopus laevis transketolase mRNA, complete cds.//1.30E-128//315aa//75%//AF270484
 TESTI20140360//XAA-PRO DIPEPTIDASE (EC 3.4.13.9) (X-PRO DIPEPTIDASE) (PROLINE DIPEPTIDASE) (PRO-
 25 LIDASE) (IMIDODIPEPTIDASE) //1.40E-55//111aa//98%//P12955
 TESTI20177400
 TESTI30000020//L.mexicana lmsap2 gene for secreted acid phosphatase 2 (SAP2) //2.00E-11//361aa//24%//Z46970
 THYMU10000020//Homo sapiens mRNA for Golgi protein (GPP34 gene) //2.20E-135//274aa//95%//AJ296152
 THYMU10000320
 30 THYMU10000830//SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT, MITOCHONDRI-
 AL PRECURSOR (EC 1.3.5.1) (FP) (FLAVOPROTEIN SUBUNIT OF COMPLEX II) //7.30E-84//185aa//87%//P31040
 THYMU10001050
 THYMU10001760//SIALOADHESIN PRECURSOR (SER) //2.50E-42//127aa//71%//Q62230
 THYMU10002910//Homo sapiens AP-4 adaptor complex beta4 subunit mRNA, complete cds. //1.30E-64//129aa//
 35 97%//AF092094
 THYMU10003290
 THYMU10003590//BETA-CHIMAERIN//2.00E-23//200aa//31%//P52757
 THYMU10003660
 THYMU10003820
 40 THYMU10004590//T-CELL-SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1) (T-CELL FACTOR 1) (TRANSCRIP-
 TION FACTOR-7) //3.70E-89//172aa//97%//Q00417
 THYMU10004730
 THYMU10004910//Homo sapiens protein serine/threonine phosphatase 4 regulatory subunit 1 (PP4R1) mRNA, com-
 plete cds. //3.70E-49//144aa//65%//AF111106
 45 THYMU10005270
 THYMU10005580//Homo sapiens Sec22 homolog mRNA, complete cds. //7.00E-139//264aa//98%//AF100749
 THYMU20001400
 THYMU20002360
 THYMU20003170//Homo sapiens topoisomerase II alpha-4 (TOP2A) mRNA, partial cds. //5.80E-09//92aa//42%//
 50 AF285159
 THYMU20003690//Mus musculus syntrophin-associated serine-threonine protein kinase mRNA, complete cds.//
 3.20E-189//481aa//73%//AF077818
 TRACH10000180
 TRACH10000300//Anabaena PCC7120 hetC gene, complete cds.//7.00E-12//200aa//29%//U55386
 55 TRACH10000570
 TRACH10000630//CDM PROTEIN (6C-AG TUMOR-ASSOCIATED ANTIGEN) (DXS1357E) //5.00E-124//246aa//
 100%//P51572
 TRACH10000740//Ig delta chain (WIE) //6.90E-251//513aa//90%//S17597

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- TRACH10001000//Oryctolagus cuniculus PIUS mRNA, complete cds.//6.50E-33//68aa//95%//U74297
- TRACH10001060
- TRACH10001250//Ig delta chain (WIE)//1.60E-233//513aa//95%//S17597
- TRACH10001400
- 5 TRACH20000150//DPP2C1//4.70E-05//152aa//30%//AAC28998
- TRACH20000790//Xenopus laevis Churchill protein mRNA, complete cds.//4.10E-47//112aa//71%//AF238862
- TRACH20001850
- TRACH20001960
- TRACH20002390
- 10 TRACH20002370//ZINC FINGER PROTEIN 184 (FRAGMENT)//5.40E-61//275aa//38%//Q99676
- TRACH20002500//HYPOTHETICAL 65.2 KDA TRP-ASP REPEATS CONTAINING PROTEIN D2030.9 IN CHROMOSOME 1//1.10E-82//375aa//42%//P90794
- TRACH20002890//GROWTH FACTOR RECEPTOR-BOUND PROTEIN 7 (GRB7 ADAPTER PROTEIN) (EPIDERMAL GROWTH FACTOR RECEPTOR GRB-7)//3.90E-188//346aa//98%//Q03160
- 15 TRACH20003930//Rattus norvegicus matrin 3 mRNA, complete cds.//4.40E-192//371aa//96%//M63485
- TRACH20004110
- TRACH20004200//MAJOR SURFACE-LABELED TROPHOZOITE ANTIGEN PRECURSOR.//4.40E-06//96aa//33%//P21849
- TRACH20004610
- 20 TRACH20004720//1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE 2 (EC 4.4.1.14) (ACC SYNTHASE 2) (S-ADENOSYL-L-METHIONINE METHYLTHIOADENOSINE-LYASE 2) (ACS-2)//5.40E-56//396aa//31%//P18485
- TRACH20004960//Rattus norvegicus kidney-specific protein (KS) mRNA, complete cds.//2.90E-282//573aa//88%//AF062399
- TRACH20004970//Transacylases//7.70E-11//151aa//32%//AAB94954
- 25 TRACH20006650//Rattus norvegicus mRNA for putative integral membrane transport protein (UST1r).//3.30E-187//552aa//62%//Y09945
- TRACH20006750//RADIAL SPOKE PROTEIN 3//1.90E-50//156aa//48%//P12759
- TRACH20007670
- TRACH20007800//homo sapiens PTH-responsive osteosarcoma B1 protein (B1) mRNA, complete cds.//8.40E-230//339aa//98%//AF095771
- 30 TRACH20008940//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//1.50E-202//384aa//97%//P53995
- TRACH20008980
- TRACH20009260//PROBABLE OXIDOREDUCTASE EPHD (EC 1.-.-.-)//5.80E-22//201aa//33%//Q10402
- TRACH20009440//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.80E-07//89aa//39%//Q05481
- 35 TRACH20011920
- TRACH20012890//SEX-LETHAL PROTEIN HOMOLOG.//1.20E-07//115aa//33%//017310 TRACH20013950//Homo sapiens NY-REN-25 antigen mRNA, partial cds.//2.20E-50//104aa//56%//AF155103
- TRACH20014000
- 40 TRACH20015920
- TRACH20016070
- UMVEN10001220
- UMVEN20001330//RABPHILIN-3A//2.00E-18//272aa//30%//P47709
- UTERU10000770//GAMETOGENESIS EXPRESSED PROTEIN GEG-154.//5.30E-33//73aa//97%//P50636
- 45 UTERU10000960//NA ATP SYNTHASE SUBUNIT H (EC 3.6.1.34) (V-ATPASE H SUBUNIT) (V-ATPASE M9.2 SUB-UNIT) (9.2 KDA MEMBRANE ACCESSORY PROTEIN).//1.60E-15//68aa//51%//015342
- UTERU1001600//ZINC FINGER PROTEIN 191//3.20E-90//346aa//52%//014754 UTERU10001920
- UTERU20000470//Homo sapiens neuropilin-2(a0) mRNA, complete cds.//5.00E-20//61aa//80%//AF022859
- 50 UTERU20003380
- UTERU20003930
- UTERU20004850//X-linked retinopathy protein//1.10E-16//97aa//51%//A46010
- UTERU20005410
- UTERU20005690

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Claims

1. A polynucleotide selected from the group consisting of the following (a) to (g):

(a) a polynucleotide comprising a protein-coding region of the nucleotide sequence of any one of SEQ ID NOs: 1 to 1639;
(b) a polynucleotide encoding a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs: 1640 to 3278;
(c) a polynucleotide comprising a nucleotide sequence encoding a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs: 1640 to 3278, wherein, in said amino acid sequence, one or more amino acids have been substituted, deleted, inserted, and/or added, and wherein said nucleotide sequence encodes a polypeptide functionally equivalent to a polypeptide comprising the selected amino acid sequence;
(d) a polynucleotide hybridizing to a polynucleotide comprising the nucleotide sequence of any one of SEQ ID NOs: 1 to 1639, wherein said nucleotide sequence encodes a polypeptide functionally equivalent to a polypeptide encoded by the selected nucleotide sequence;
(e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a polypeptide encoded by the polynucleotide according to any one of (a) to (d);
(f) a polynucleotide comprising a nucleotide sequence having at least 70% identity to the nucleotide sequence of any one of SEQ ID NOs: 1 to 1639; and
(g) a polynucleotide comprising a nucleotide sequence having at least 90% identity to the nucleotide sequence of any one of SEQ ID NOs: 1 to 1639.

2. A polypeptide encoded by the polynucleotide of claim 1, or a partial peptide thereof.

3. An antibody binding to the polypeptide or the peptide of claim 2.

4. A method for immunologically assaying the polypeptide or the peptide of claim 2, said method comprising the steps of contacting the polypeptide or the peptide of claim 2 with the antibody of claim 3, and observing the binding between the two.

5. A vector comprising the polynucleotide of claim 1.

6. A transformant carrying the polynucleotide of claim 1 or the vector of claim 5.

7. A transformant carrying the polynucleotide of claim 1 or the vector of claim 5 in an expressible manner.

8. A method for producing the polypeptide or the peptide of claim 2, said method comprising the steps of culturing the transformant of claim 7 and recovering an expression product.

9. An oligonucleotide comprising at least 15 nucleotides, said oligonucleotide comprising a nucleotide sequence complementary to the nucleotide sequence of any one of SEQ ID NOs: 1 to 1639 or to a complementary strand thereof.

10. Use of the oligonucleotide of claim 9 as a primer for synthesizing the polynucleotide of claim 1.

11. Use of the oligonucleotide of claim 9 as a probe for detecting the polynucleotide of claim 1.

12. An antisense polynucleotide against the polynucleotide of claim 1 or a part thereof.

13. A method for detecting the polynucleotide of claim 1, said method comprising the following steps of:

a) incubating a target polynucleotide with the oligonucleotide of claim 9 under hybridizable conditions, and
b) detecting hybridization of the target polynucleotide with the oligonucleotide of claim 9.

14. A database of polynucleotides and/or polypeptides, said database comprising information on at least one of the nucleotide sequences of SEQ ID NOs: 1 to 1639 and/or on at least one of the amino acid sequences of SEQ ID NOs: 1640 to 3278.

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Figure 1

